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GAATTCGGAG GAATTATTC AATCATAAAC ACAAATAAAC ATTTCAGTAG TTCCCCACAA	60
CACACACACA CACAGCCCCG GCAITATTAC ACTAAALGCC ACACATCAATC CAAAMAAATCA	120
GCACCAAAAA CATCAATAAA C ATC CAT TCC ATT AAA TGT TTA TTA ACA GCA	171
Met His Trp Ile Lys Cys Leu Leu Thr Ala	10
TTC ATT TCC TTC ACA GTC ATC GTC CAC GTT CAC AGT TCC GCC ACC TTT	219
Phe Ile Cys Phe Thr Val Ile Val Glu Val His Ser Ser Gly Ser Phe	25
CAC TTC CCC CTC AAC TAC TTC ACC AAC CAT CAC CCC CGG CAC AAC CAC	267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asn His Gly Arg Asn Asn Glu	40
GGT CCC TCC TCC ACC GCG CAC TCC CAC CGA CCG ACC CCC AAC TCC CTC	315
Gly Arg Cys Cys Ser Gly Glu Ser Asn Gly Ala Thr Gly Lys Cys Leu	55
CCC ACC TCC AAC ACC GCG TTT CCG CTC TCC CTA AAC CAC TAC CAC CCC	363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Glu Ala	70
AAC ATC CAC ACC ACC TCC CAC TCC ACC TAC GCG CAC CTC ATC ACC CCC	411
Thr Ile Asn Thr Thr Ser Glu Cys Thr Tyr Gly Asn Val Ile Thr Pro	90
ATT CTC GCG CAC AAC TCC GTC AAT CTC ACC CAC CCC CAC CCC TTC CAC	459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asn Ala Glu Arg Phe Glu	105
AAC AAC GCG TTC ACC AAT CCC ATC CAC TTC CCC TTC TCC TTC TCA TCC	507
Asn Lys Gly Phe Thr Asn Pro Ile Glu Phe Pro Phe Ser Phe Ser Trp	120
CCG GGT ACC TTC TCC CTC ATC CTC CAC CCC TCC CAT CAT ACC AAC AAT	555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asn Thr Asn Asn	135
ACC GCG AAT GCG CGA ACC AAC AAC CTC CTC ATC CAC CGA CTC TTC GTC	603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Glu Arg Leu Leu Val	150
CAC CAC GTA CTC CAC CTC TCC TCC CAA TCC AAC ACC AAC AAC TCC CAA	651
Glu Glu Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu	170
TCC CAC TAC ACC TCC CTC CAC TAC CAT TTC CGT CTC ACC TCC CAT CTC	699
Ser Glu Tyr Thr Ser Leu Glu Tyr Asn Phe Arg Val Thr Cys Asn Leu	185
AAC TAC TAC GGA TCC GCG TGT CCC AAC TTC TCC CCG CCC CCG CAC CAT	747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asn Asn	200
TCA TTT CCA CAC TCC ACT TCC TCC CAC ACC GCG CAA ATT ATC TGT TTC	795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu	215
ACC CCA TCC CAC GCG CAT TAC TGT CAC ATA CCC AAA TCC GCG AAA GCG	843
Thr Gly Trp Glu Gly Asn Tyr Cys His Ile Pro Lys Cys Ala Lys Gly	230
TGT CAA CAT CCA CAT TCC CAC AAA CCC AAT CAA TCC GTT TCC CAA CTC	891
Cys Glu His Gly His Cys Asn Lys Pro Asn Glu Cys Val Cys Glu Leu	250

Figure 1 Cont'D

CCC TCC AAC CCA GCC TTC TCC AAC CAC TCC GTT CTC GAA CCG AAC TCC Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys 255 260 265	939
ATC CAT CCC ACC TCC AAC AAA CCC TCC ACT TCC ATC TCC AAC CAC CCT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly 270 275 280	987
TCC GCA CCC TTC TAC TCC AAC CAC CAT CTC AAC TAC TCC ACC AAC CAC Trp Gly Gly Leu Tyr Cys Asn Glu Asn Leu Asn Tyr Cys Thr Asn His 285 290 295	1035
ACA CCC TCC AAC AAT GCC GCA ACC TCC TTC AAC ACC GCC CAC CCA TTC Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu 300 305 310	1083
TAC ACA TCC AAA TCC CCT CCA CCA TAC AGT CGT CAT CAT TCC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asn Asn Cys Glu Asn 315 320 325 330	1131
CAC ATC TAC TCC TCC GAT CCC GAT GTC AAT CCC TCC CAC AAT CCT CCT Glu Ile Tyr Ser Cys Asn Ala Asn Val Asn Pro Cys Glu Asn Gly Gly 335 340 345	1179
ACC TCC ATC GAT CAC CCC CAC ACA AAA ACC CCC TAC AAC TGT CAT TCC Thr Cys Ile Asn Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys 350 355 360	1227
CCC AAC CCC TCC ACC GCA AAC ATC TCC CAC CAC AAA CTC CTC ACC TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys 365 370 375	1275
TCC CAC AAA CCC TGT CAT CAC GCA ATC TCC CCC AAC GTT CCT CCT CCC Ser Asn Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly 380 385 390	1323
TTC GCA ACC AAC CCT CAC GGC TAC CAC TCC GAA TGT CCC ATT CCC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr 395 400 405 410	1371
ACC GCA CCC AAC TCC CAT CTC CAC CTC CAC AAC TCC AGT CCC AAT CCA Ser Gly Pro Asn Cys Asn Leu Gln Leu Asn Asn Cys Ser Pro Asn Pro 415 420 425	1419
TCC ATA AAC GGT CCA ACC TGT CAC CCC ACC GCA AAC TGT ATT TCC CCA Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro 430 435 440	1467
CCC GCA TTT TCC GCA ACC ACA TCC CAC ACC AAC ATT CAC CAT TGT CTT Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asn Asn Cys Leu 445 450 455	1515
CCC CAC CAC TCC CAC AAC GCA CCC ACC TCC ATA CAT ATC GTC AAC CAA Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asn Met Val Asn Gln 460 465 470	1563
TAT CCC TCC CAA TCC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT ACC Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser 475 480 485 490	1611
AAA GTT CAC TTC TCC CTC ATC ACA CCC TGT CCC AAT CCA CCA ACC TCC Lys Val Asn Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys 495 500 505	1659
TTC AAT CTC AAC AAC CAT TAC CAC TCC ACC TGT CCT CCC GCA TTT ACT Leu Asn Leu Asn Asn Asn Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr 510 515 520	1707

Figure 1 Cont'D

GGG	AAG	GAT	TGC	TCT	GTC	GAC	ATC	GAT	GAG	TCC	ACC	AGT	CGA	CCC	TGT	1755
Gly	Lys	Asp	Cys	Ser	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	
		525					530					535				
CAT	AAC	GCC	GCC	ACT	TCC	ATC	AAC	CGC	GTC	AAT	TCC	TTC	CAA	TCC	GTC	1803
His	Asn	Gly	Gly	Thr	Cys	Met	Asn	Arg	Val	Asn	Ser	Phe	Glu	Cys	Val	
		540				545					550					
TGT	CCC	AAT	GGT	TTC	ACG	GCC	AAC	CAG	TCC	GAT	CAG	GAG	TCC	TAC	GAT	1851
Cys	Ala	Asn	Gly	Phe	Arg	Gly	Lys	Gln	Cys	Asp	Glu	Glu	Ser	Tyr	Asp	
		555			560					565					570	
TCC	GTC	ACC	TTC	GAT	GCC	CAC	CAA	TAT	CCA	GCC	ACC	ACA	CAA	GCC	ACA	1899
Ser	Val	Thr	Phe	Asp	Ala	His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	
				575					580					585		
CCC	GAT	GGT	TTC	ACC	AAT	GCC	CAG	GTA	GTC	GTA	ATT	GCT	GTT	TTC	TCC	1947
Ala	Asp	Gly	Leu	Thr	Asn	Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	
			590					595					600			
GTT	CCC	ATC	CCT	TTC	GTC	GCC	GTT	ATT	GCC	GCC	TCC	GTC	GTC	TTC	TCC	1995
Val	Ala	Met	Pro	Leu	Val	Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	
		605					610					615				
ATC	AAC	CGC	AAC	CGT	AAC	CGT	CAG	CAA	AAC	CAC	CAC	GCC	CAC	GCC		2043
Met	Lys	Arg	Lys	Arg	Lys	Arg	Ala	Gln	Glu	Lys	Asp	Asp	Ala	Glu	Ala	
		620				625					630					
ACG	AAC	CAG	AAC	CAA	CAG	AAT	GCC	GTC	GCC	ACA	ATC	CAT	CAC	AAT	GCC	2091
Arg	Lys	Gln	Asn	Glu	Gln	Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	
		635			640					645					650	
AGT	GGC	GTC	GGT	GTA	GCT	TTC	GCT	TCA	GCC	TCT	CTC	GGC	GGC	AAA	ACT	2139
Ser	Gly	Val	Gly	Val	Ala	Leu	Ala	Ser	Ala	Ser	Leu	Gly	Gly	Lys	Thr	
				655					660					665		
GGC	ACC	AAC	AGC	GGT	CTC	ACC	TTC	GAT	GCC	GCC	AAC	CCG	AAT	ATC	ATC	2187
Gly	Ser	Asn	Ser	Gly	Leu	Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	
			670					675					680			
AAA	AAC	ACC	TGC	GAC	AAC	TCC	GTC	AAC	AAC	ATT	TGT	GCC	TCA	CCA	CCA	2235
Lys	Asn	Thr	Trp	Asp	Lys	Ser	Val	Asn	Asn	Ile	Cys	Ala	Ser	Ala	Ala	
		685					690					695				
CCA	GCC	GCC	GCC	GCC	GCA	GCA	GCC	GCC	CAC	GAC	TGT	CTC	ATG	TAC	GCC	2283
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Glu	Cys	Leu-Met	Tyr	Gly		
		700				705					710					
CGA	TAT	GTC	GCC	TCC	GTC	GCC	GAT	AAC	AAC	AAT	GCC	AAC	TCA	CAC	TTC	2331
Gly	Tyr	Val	Ala	Ser	Val	Ala	Asp	Asn	Asn	Asn	Ala	Asn	Ser	Asp	Phe	
		715			720					725					730	
TGT	GTC	GCT	CCG	CTA	CAA	AGA	GCC	AAC	TCC	CAA	AAC	CAA	CTC	AAC	ACC	2379
Cys	Val	Ala	Pro	Leu	Gln	Arg	Ala	Lys	Ser	Gln	Lys	Gln	Leu	Asn	Thr	
			735					740					745			
GAT	CCC	ACC	CTC	ATG	CAC	CGC	GGT	TCC	CCG	GCA	GGC	AGC	TCA	GCC	AAC	2427
Asp	Pro	Thr	Leu	Met	His	Arg	Gly	Ser	Pro	Ala	Gly	Ser	Ser	Ala	Lys	
			750				755					760				
CGA	CCC	TCT	GCC	CGA	CGA	CCC	CGA	CCC	CCC	CAC	GGC	AAC	AGC	ATC	TCT	2475
Gly	Ala	Ser	Gly	Gly	Gly	Pro	Gly	Ala	Ala	Glu	Gly	Lys	Arg	Ile	Ser	
		765				770						775				
GTT	TTA	GCC	CAC	GCT	TCC	TAC	TGT	AGC	CAC	CGT	TCC	CCC	TCC	TTC	CCC	2523
Val	Leu	Gly	Glu	Gly	Ser	Tyr	Cys	Ser	Gln	Arg	Trp	Pro	Ser	Leu	Ala	
		780				785					790					

Figure 1 Cont'D

CCC CCG CCA CTC CCC CCA CCC TGT TCA TCC CAG CTA ATC GCT CCA CCT	2571
Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Glu Leu Met Ala Ala Ala	
795 000 005 010	
TCG CCA CCG GCG ACC CCA CCG CCG ACC GCG CAA CAG CAG CCA TCC CTC	2619
Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Glu Glu Glu Arg Ser Val	
015 020 025	
CTC TCC GCG ACT CCC CAT ATG TAACTCCAAA AATCCCGAAG CCGTCCCTCT	2670
Val Cys Gly Thr Phe His Met	
030	
AAATCCGCAG AAATCCGCAT CCAAGAGCTC ACAGCAGATA CACAAACAAA ACACCTGGGT	2730
GGCTTC AAAA TGTGAGAGAG AGCCCAAAAT GTTCTTCTTG ATTGAAAGCAG TTTAGTCTC	2790
ACGAAAAATC AAAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAAATTACCA AGCTGTGACC CAGCCGTTTC CATCCCGAAT TC	2892

Figure 2

		% Aggregation with DI with Ser	
1. pMIMg		40	21
2. ΔSph		0	nl
3. ΔCln		0	nl
4. ΔEGF(7-17)		0	nl
5. ΔEGF(9-26)		0	nl
6. ΔEGF(17-30)		22	nl
7. ΔEGF(7-9)		20	14
8. ΔEGF(9-17)		0	0
9. ΔEGF(17-26)		10	8
10. ΔEGF(26-30)		5	7
11. ΔEGF(9-30)		0	nl
12. ΔEGF(7-26)		0	nl
13. ΔCln+EGF(9-17)		35	20
14. ΔCln+EGF(17-26)		0	nl
15. split		42	nl
16. ΔCln+EGF(9-13)		47	25
17. ΔCln+EGF(11-15)		0	0
18. ΔCln+EGF(13-17)		0	nl
19. ΔCln+EGF(10-13)		56	23
20. ΔCln+EGF(11-13)		0	nl
21. ΔCln+EGF(10-12)		0	nl
22. ΔCln+EGF(10-11)		0	nl
23. ΔCln+EGF(10-12)		45	nl
24. ΔCln+EGF(11-12)		11	nl
25. ΔEGF		0	nl
26. ΔEGF+EGF(9-17)		24	nl
27. ΔEGF+EGF(9-13)		40	nl
28. ΔEGF+EGF(10-13)		45	23
29. ΔEGF+EGF(10-12)		48	nl
30. ΔECN		0	nl
31. ΔECN+EGF(10-13)		26	nl
32. ΔECN+EGF(10-12)		47	22
33. ΔCln+ΔEGF(10-13)		42	20

Figure 3

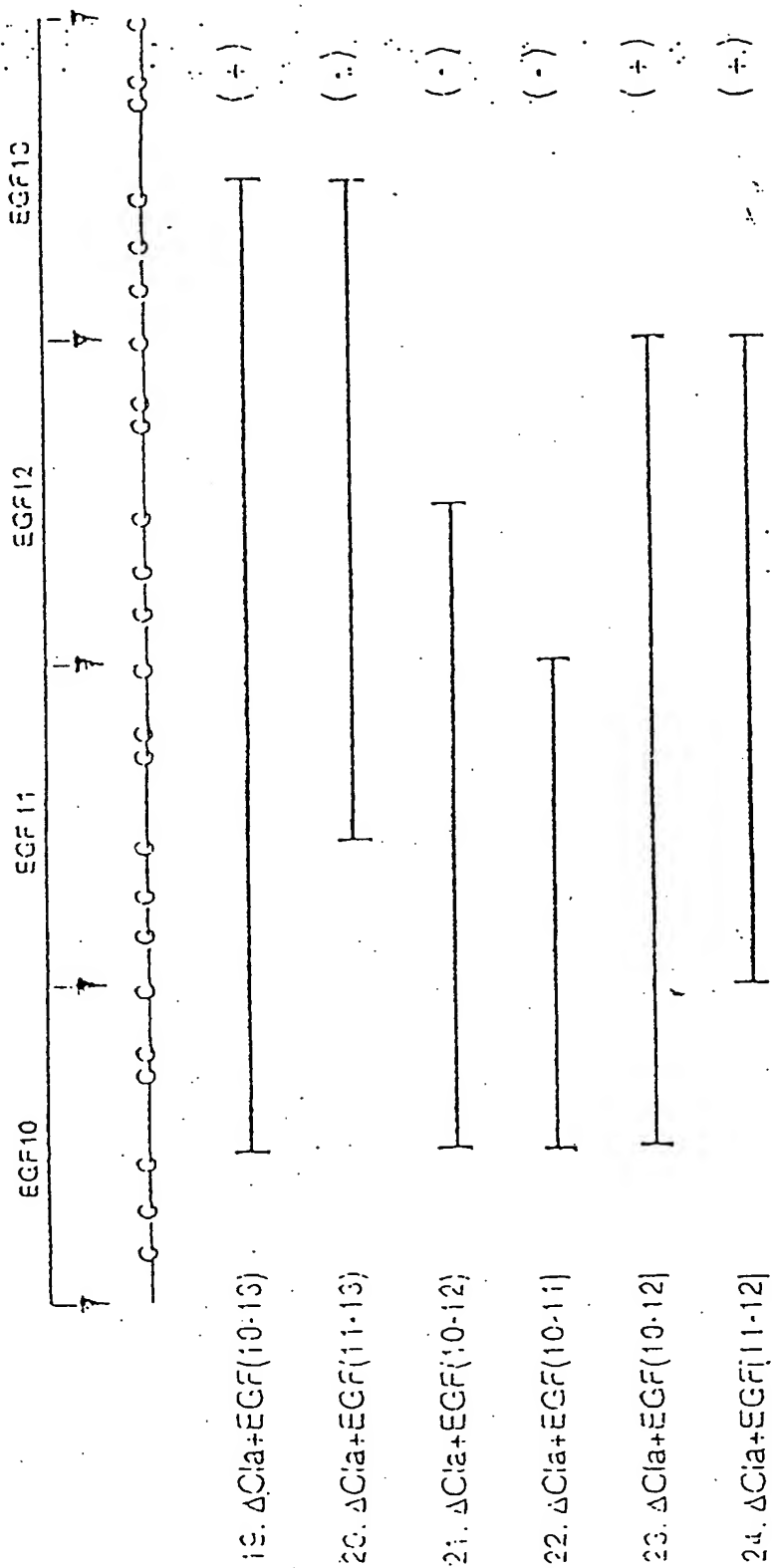
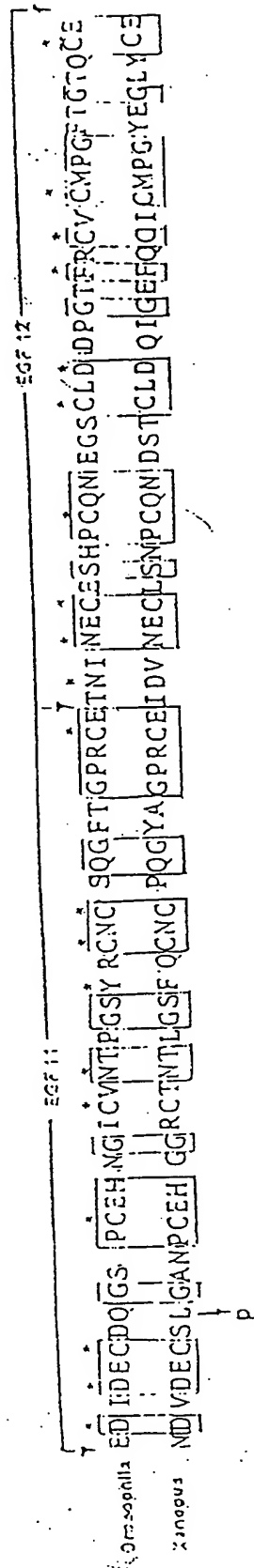


Figure 4



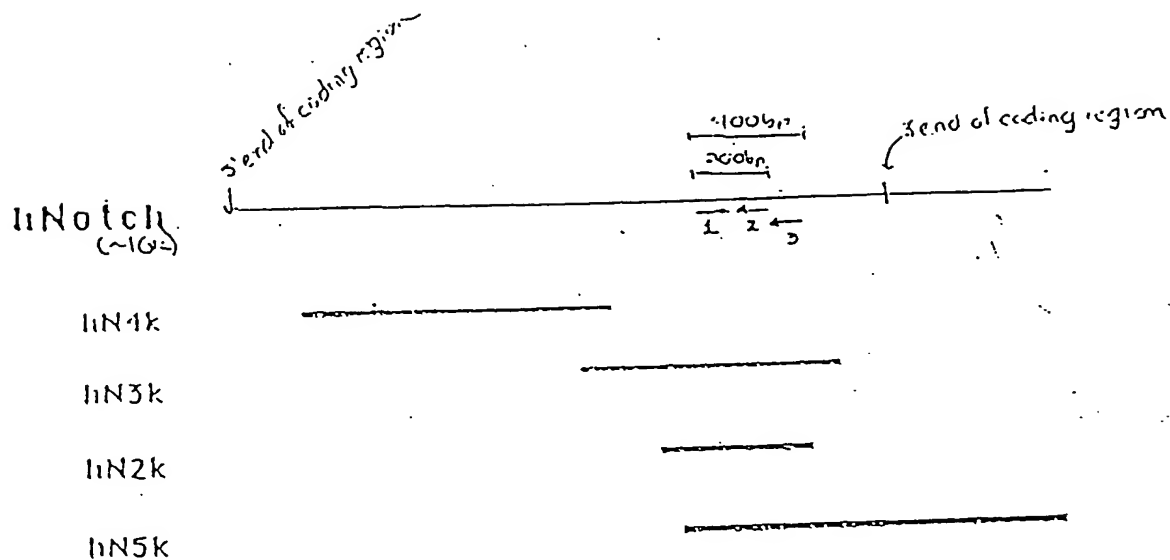


Figure 6

Figure 7

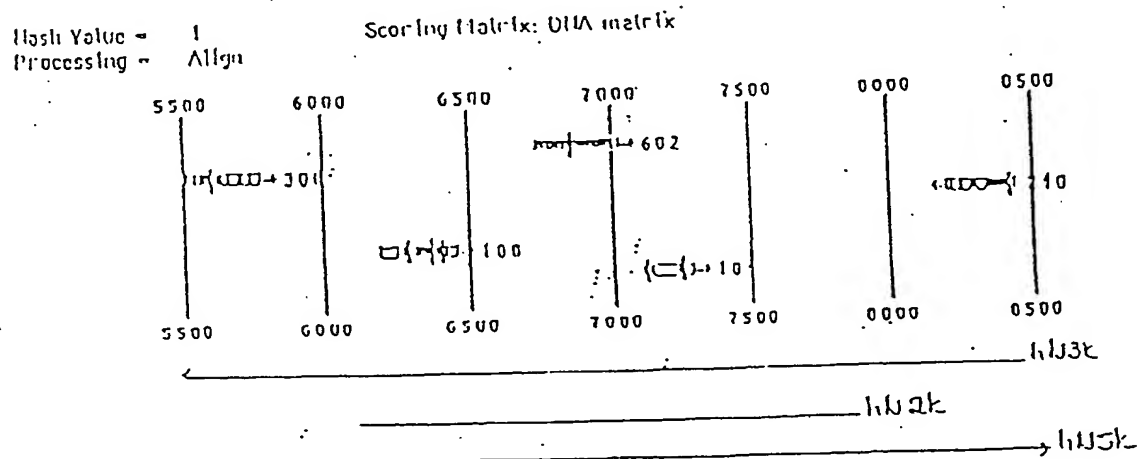
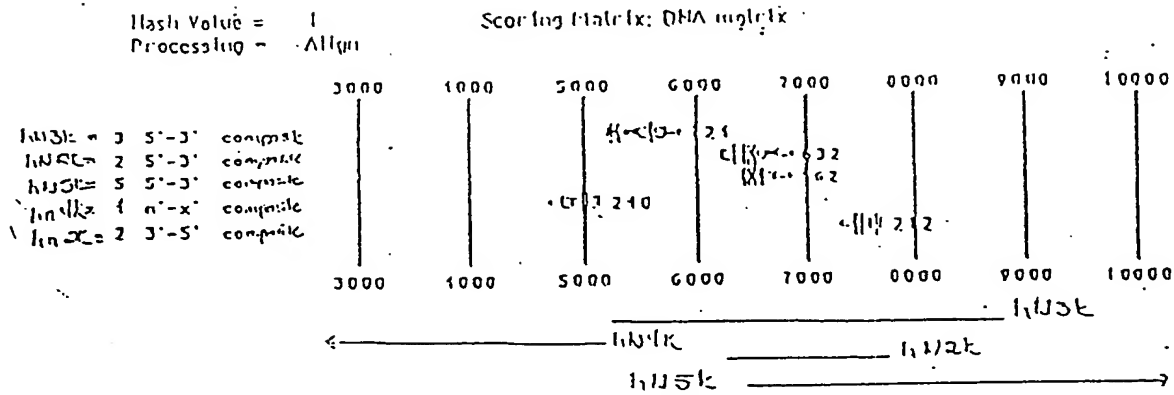


Figure 8A

A.

```

1  GAAATCCGCT GGGAGGAAATGG TCTGAGCTAC CTGCCCCGTCC TGCTGGGGCA TCANTGGCAH
61  GTGGGGGAAAG CCRCACTGGG CAAACGGGCC AGGCCAATTC TGGAAATGTG TACATGGTGG
121  GCAGGGGGGCC CGCAGCAGCT GCGAGGCGAGG TGGACTGAGG CTGGGGATCC CCGCTGCTT
181  GGGCAATAGT GCGTTTACCC ATGAGCTGGH AAGTCACAAI GGGGGGCAAG GGTCCCGAG
241  GGTGGTATG TGCTTCCTTC AGGTGGC

```

Figure 8B

B.

```

1  GAAATCCCTC CATATATAGT GACTTTTCTG AARCTGAGC CACCCCTAGTG TCCTTAACTC
61  CCTCTGGAGT TTGTAGCTT TGGTCTTTC AAGAGCGAGG CTCTCTTCAH GCTCCTTAAT
121  GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACTT TTGGTAATTC ATTCTTCTTC
181  AACCCCGAAC TGAGGCTGG CTCTCACTCT CTAGGCAAGG CAGGAAATCC GAGGTGGATG
241  TGTTAGATGT GAATGTCCGT GGGCCAGATG GCTGCACCCC ATTAGATGTG GCTTCTCTCC
301  GAGGAGGCCAG CTCAGATTTG AGTCATCAAG ATCAAGATCC AGAGCACTCT TCTGCTAACA
361  TCATCAGAGA CTGGGTCTAC CAGGGTGCCA GCTCCAGHC CAGACAGACC GGACTGCTGA
421  GATGGCCCTG CACCTTGCAG CCGCTTACTC AGGGGCTGAT GCTGCCAGGC GTCTCTCTGA
481  TGCAGGTGCA GATGCCAATG CCGAGGACAA CATGGGCCGC TGTCACATCC ATGCTGCAGT
541  GGCACGTGAT GGCAGGTGT ATTCAAGTCT GTTA

```

Figure 8C

C.

```

1  TCCAGATICT GATTCGCAGC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA
61  CACCCCTGAT CCTGGCTGCC CCGCTGGCTG TGGAGCGAAT GGTGCCAGAA CTGATCAACT
121  GCGAGCGGGA TGTGAATGCA GTGGATGACC ATCGAATAAT TCTCTTAC TGGGCACTG
181  CTGTCAATAA TGTGGAGGCA ACCTTTTTGT TGTGAAAAA TGGGGCCAGC CCGAGCATGC
241  AGCAGACAAA GGAAGAGACA CCTCTGTTC TTGCTGCCCG GGAGGAGCTA TAGG

```

Figure 9A

```

1  GAATTCATTT CAGGAGGAAA GGGTGGGGAG ACNAGCAGGC ACCCACTTTC CCGTGGCTGG
61 ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CCGAGTGCCA
121 TTCAGAAAT TCCAGAAAG CCGTACCCCA ACTCGGACGG CAGAGTCACA CCCCTGGCTA
181 GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGACGGG GGGATGGCAC CCCCTGCAGG
241 CAGAGCTG

```

Figure 9B

```

1  CTAAAGGGAA CAAAGGCHGG AGCTCCACCC CGGGCGGCHC HGCTCTAGAA CTAGTGGANH
61 HCCCGGGCTG CAGGAATTC GGGGACTGG GCTCGGGCTC AGAGCGGCGC TGTGACAGG
121 ATTCTAGACC GGGAGAGCAA GCGATGGCT GACAGCTGGC CTCCAAAGTC ACCAGGCTCA
181 ATCCTCTGGC CCGGACATC GAGCGATGCA GAGGATCAGA ACCGGTACCT GAGTGGCATG
241 ACTCGGATTT ACAAGCATGA CAGCGCTGCT TACAGGGAGC GTGAHHITTT CACATGCAGT
301 CGACAGACAC GAGCTCTATG CAT

```

Figure 10

7326-131

10 20 30 40
 TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC
 C Q E D A G N K V C S L Q C N N>
 50 60 70 80 90
 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC
 H A C G W D G G D C S L N F N D>
 100 110 120 130 140
 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT
 P W K N C T Q S L Q C W K Y F S>
 150 160 170 180 190
 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC
 D G H C D S Q C N S A G C L F D>
 200 210 220 230 240
 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC
 G F D C Q R A E G Q C N P L Y D>
 250 260 270 280
 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC
 Q Y C K D H F S D G H C D Q G C>
 290 300 310 320 330
 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA
 N S A E C E W D G L D C A E H V>
 340 350 360 370 380
 CCC GAG AGG CTG GCG GCC GGC ACG CTG GTG GTG GTG GTG CTG ATG CCG
 P E R L A A G T L V V V V L M P>
 390 400 410 420 430
 CCG GAG CAG CTG CGC AAC AGC TCC TTC CAC TTC CTG CGG GAG CTC AGC
 P E Q L R N S S F H F L R E L S>
 440 450 460 470 480
 CGC GTG CTG CAC ACC AAC GTG GTC TTC AAG CGT GAC GCA CAC GGC CAG
 R V L H T N V V F K R D A H G Q>
 490 500 510 520
 CAG ATG ATC TTC CCC TAC TAC GGC CGC GAG GAG GAG CTG CGC AAG CAC
 Q M I F P Y Y G R E E E L R K D>
 530 540 550 560 570
 CCC ATC AAG CGT GCC GCC GAG GGC TGG GCC GCA CCT GAC GCC CTG CTG
 P I K R A A E G W A A P D A L L>

```

580      590      600      610      620
GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CGG
G   Q   V   K   A   S   L   L   P   G   G   S   E   G   G   R>

630      640      650      660      670
CGG GGG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC
R   R   R   E   L   D   P   M   D   V   R   G   S   I   V   Y>

680      690      700      710      720
CTG GAG ATT GAC AAC CGG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC
L   E   I   D   N   R   Q   C   V   Q   A   S   S   Q   C   F>

730      740      750      760
CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG
Q   S   A   T   D   V   A   A   F   L   G   A   L   A   S   L>

770      780      790      800      810
GGC AGC CTC AAC ATC CCC TAC AAG ATC GAG GCC GTG CAG AGT GAG ACC
G   S   L   N   I   P   Y   K   I   E   A   V   Q   S   E   T>

820      830      840      850      860
GTG GAG CCG CCC CCG CCG GCG CAG CTG CAC TTC ATG TAC GTG GCG GCG
V   E   P   P   P   P   A   Q   L   H   F   M   Y   V   A   A>

870      880      890      900      910
GCC GCC TTT GTG CTT CTG TTC TTC GTG GGC TGC GGG GTG CTG CTG TCC
A   A   F   V   L   L   F   F   V   G   C   G   V   L   L   S>

920      930      940      950      960
CGC AAG CGC CGG CGG CAG CAT GGC CAG CTC TGG TTC CCT GAG GGC TTC
R   K   R   R   R   Q   H   G   Q   L   W   F   P   E   G   F>

970      980      990      1000
AAA GTG TCT GAG GCC AGC AAG AAG AAG CGG CGG GAG CCC CTC GGC GAG
K   V   S   E   A   S   K   K   K   R   R   E   P   L   G   E>

1010      1020      1030      1040      1050
GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC
D   S   V   G   L   K   P   L   K   N   A   S   D   G   A   L>

1060      1070      1080      1090      1100
ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG
M   D   D   N   Q   N   E   W   G   D   E   D   L   E   T   K>

1110      1120      1130      1140      1150
AAG TTC CGG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG
K   F   R   F   E   E   P   V   V   L   P   D   L   D   D   Q>

1160      1170      1180      1190      1200

```

ACA GAC CAC CGG CAG TGG ACT CAG CAG CAC CTG GAT GCC GGT GAC CTG
 T D H R Q W T Q Q H L D A A D L>

1210 1220 1230 1240
 CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC
 R M S A M A P T P P Q G E V D A>

1250 1260 1270 1280 1290
 GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC
 D C M D V N V R G P D G F T P L>

1300 1310 1320 1330 1340
 ATG ATC GCC TCC TGC AGC GGG GGC GGC CTG GAG ACG GGC AAC AGC GAG
 M I A S C S G G G L E T G N S E>

1350 1360 1370 1380 1390
 GAA GAG GAG GAC GCG CCG GCC GTC ATC TCC GAC TTC ATC TAC CAG GGC
 E E E D A P A V I S D F I Y Q G>

1400 1410 1420 1430 1440
 GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC
 A S L H N Q T D R T G E T A L H>

1450 1460 1470 1480
 CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG
 L A A R Y S R S D A A K R L L E>

1490 1500 1510 1520 1530
 GCC AGC GCA GAT GCC AAC ATC CAG GAG AAC ATG GGC CGC ACC CCG CTG
 A S A D A N I Q D N M G R T P L>

1540 1550 1560 1570 1580
 CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC
 H A A V S A D A Q G V F Q I L I>

1590 1600 1610 1620 1630
 CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG
 R N R A T D L D A R M H D G T T>

1640 1650 1660 1670 1680
 CCA CTG ATC CTG GCT GCC CGC CTG GCC GTG GAG GGC ATG CTG GAG GAC
 P L I L A A R L A V E G M L E D>

1690 1700 1710 1720
 CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG
 L I N S H A D V N A V D D L G E>

1730 1740 1750 1760 1770
 TCC GCC CTG CAC TGG GCC GCC GCC GTG AAC AAT GTG GAT GCC GCA GTT
 S A L H W A A A V H H V D A A V>

1780	1790	1800	1810	1820
GTG CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG				
V L L K N G A N K D M Q N N R E>				
1830	1840	1850	1860	1870
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCG				
E T P L F L A A R E G S Y E T A>				
1880	1890	1900	1910	1920
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT AFG				
K V L L D H F A N R D I T D H M>				
1930	1940	1950	1960	
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC				
D R L P R D I A Q E R M H H D I>				
1970	1980	1990	2000	2010
GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC				
V R L L D E Y N L V R S P Q L H>				
2020	2030	2040	2050	2060
GGA GCC CCG CTG GGG GGC ACG CCC ACC CTG TCG CCC CCG CTC TGC TCG				
G A P L G G T P T L S P P L C S>				
2070	2080	2090	2100	2110
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG				
P N G Y L G S L K P G V Q G K K O>				
2120	2130	2140	2150	2160
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC				
V R K P S S K G L A C G S K E A>				
2170	2180	2190	2200	
AAG GAC CTC AAG GCA CGG AAG AAG AAG TCC CAG GAT GGC AAG GGC TGC				
K D L K A R R K K S Q D G K G C>				
2210	2220	2230	2240	2250
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA				
L L D S S G M L S P V D S L E S>				
2260	2270	2280	2290	2300
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC				
P H G Y L S D V A S P P L L P S>				
2310	2320	2330	2340	2350
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG				
P F Q Q S P S V P L H H L P G M>				
2360	2370	2380	2390	2400

Figure 10 Cont'D

CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC
 P D T H L G I G H L N V A A K P>

2410 2420 2430 2440
 CAG ATG GCG GCG CTG GGT GGG GGC GGC CGG CTG GCC TTT GAG ACT GGC
 E M A A L G G G G R L A F E T G>

2450 2460 2470 2480 2490
 CCA CCT CGT CTC TCC CAC CTG CCT GTG GCC TCT GGC ACC AGC ACC GTC
 P P R L S H L P V A S G T S T V>

2500 2510 2520 2530 2540
 CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GGC GGG TCC
 L G S S S G G A L N F T V G G S>

2550 2560 2570 2580 2590
 ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC
 T S L N G Q C E W L S R L Q S G>

2600 2610 2620 2630 2640
 ATG GTG CCG AAC CAA TAC AAC CCT CTG CGG GGG AGT GTG GCA CCA GGC
 M V P N Q Y N P L R G S V A P G>

2650 2660 2670 2680
 CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG
 P L S T Q A P S L Q H G M V G P>

2690 2700 2710 2720 2730
 CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC
 L H S S L A A S A L S Q M M S Y>

2740 2750 2760 2770 2780
 CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG
 Q G L P S T R L A T Q P H L V Q>

2790 2800 2810 2820 2830
 ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG
 T Q Q V Q P Q N L Q M Q Q Q N L>

2840 2850 2860 2870 2880
 CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA
 Q P A H I Q Q Q Q S L Q P P P P>

2890 2900 2910 2920
 CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG
 P P Q P H L G V S S A A S G H I>

2930 2940 2950 2960 2970
 GGC CGG AGC TTC CTG AGT GCA GAG CCG AGC CAG GCA GAC GTG CAG CCA

Figure 10 Cont'D

G R S F L S G E P S Q A D V Q P>
 2980 2990 3000 3010 3020
 CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC
 L G P S S L A V H T I L P Q E S>
 3030 3040 3050 3060 3070
 CCC GCC CTG CCC ACG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC
 P A L P T S L P S S L V P P V T>
 3080 3090 3100 3110 3120
 CCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT
 A A Q F L T P P S Q H S Y S S P>
 3130 3140 3150 3160
 GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG
 V D N T P S H Q I Q V P V P V M>
 3170 3180 3190 3200 3210
 GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC
 V M I R S S D P S K G S S I L I>
 3220 3230
 GAA GCT CCC GAC TCA TGG
 E A P D S W>

Figure 11

7326-131

G GAG GTG GAT GTG TTA GAT GTG AAT GTG CCT GCG CCA GAT GCG TCG Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Phe Asp Gly Cys 1 5 10 15	46
ACC CCA TTC ATG TGC GGT TGT CTC CCA CCA GCG AGC TCA GAT TTC ACT Thr Phe Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser 20 25 30	94
GAT GAA GAT GAA GAT CCA GAG GAC TCT TCT GGT AAC ATC ATC ACA GAG Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp 35 40 45	142
TTC CTC TAC GAG GGT GCG AAC CTC GAG GCG CAG ACA GAG CCG ACT GGT Leu Val Tyr Glu Gly Ala Ser Leu Glu Ala Glu Thr Asp Arg Thr Gly 50 55 60	190
GAG ATG GCG CTC GAG GTT CCA GCG GCG TAC TCA CCG GGT GAT GGT GCG Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala 65 70 75	230
AAC GGT CTC CTC GAT CCA GGT CCA GAT GCG AAT GCG CAG GAG AAC ATC Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Glu Asp Asn Met 80 85 90 95	286
GCG GCG TGT CCA CTC GAT GGT CCA CTC CCA GCT GAT GCG CAA GGT CTC Gly Arg Cys Phe Leu His Ala Ala Val Ala Ala Asp Ala Glu Gly Val 100 105 110	334
ATC CAG ATT CTC ATT CCG AAC CGA GTA ACT GAT GTA GAT GCG AGG ATC Phe Glu Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met 115 120 125	382
AAT GAT GGT ACT ACA CCG CTC ATC CTC GGT GCG CCG CTC GGT CTC GAG Asn Asp Gly Thr Thr Phe Leu Ile Leu Ala Ala Arg Leu Ala Val Glu 130 135 140	430
GCA ATC CTC CCA GAA CTC ATC AAC TCG CAA CCG GAT CTC AAT CCA CTC Gly Met Val Ala Glu Leu Ile Asn Cys Glu Ala Asp Val Asn Ala Val 145 150 155	478
GAT GAG GAT CCA AAA TCT GGT GTT GAG TCG CCA GGT GGT CTC AAT AAT Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Val Asn Asn 160 165 170 175	526
CTC GAG CCA ACT GTT TTG TTG TTG AAA AAT GCG CCG AAC CCA GAG ATC Val Glu Ala Thr Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met 180 185 190	574
CAG GAG AAC AAC CAA GAG ACA CCT CTC TTT GTT GGT CCG CCG GAG GCG Glu Asp Asn Lys Glu Glu Thr Phe Leu Phe Leu Ala Ala Arg Glu Gly 195 200 205	622
AGC TAT CAA CCA GCG AAC ATC CTC TTA GAG GAT TTT CCG AAT CCA GAG Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp 210 215 220	670
ATC ACA GAG GAT ATC GAT GGT GTT CCG CCG GAT CTC GGT CCG GAT CCG Ile Thr Asp His Met Asp Arg Leu Phe Arg Asp Val Ala Arg Asp Arg 225 230 235	718
ATC CAG CAT GAG ATT CTC CCG GTT CTC GAT CAA TAC AAT CTC ACC CCA Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Phe 240 245 250 255	766

Figure 11 Cont'D

ACC	CCT	CCA	CCC	ACC	GTC	TTG	ACT	TCT	GCT	CTC	TCA	CCT	GTC	ATC	TGT	014
Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Val	Ile	Cys	
				260					265					270		
CCC	CCC	AAC	ACA	TCT	TTC	CTC	AGC	CTG	AAG	CAC	ACC	CCA	ATG	CCC	AAG	062
Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His	Thr	Pro	Met	Gly	Lys	
			275					280					285			
AAG	TCT	ACG	CCC	CCC	AGT	CCC	AAC	AGT	ACC	ATG	CCT	ACT	ACC	CTC	CCT	310
Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met	Pro	Thr	Ser	Leu	Pro	
			290				295					300				
AAC	CTT	CCC	AAG	CAG	CCA	AAG	CAT	CCC	AAG	CCT	ACT	AGG	AGG	AAG	AAG	950
Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly	Ser	Arg	Arg	Lys	Lys	
			305			310					315					
TCT	CTG	AGT	CAC	AAG	GTC	CAA	CTG	TCT	CAC	AGT	TCA	GTA	ACT	TTA	TCC	1006
Ser	Leu	Ser	Glu	Lys	Val	Glu	Leu	Ser	Glu	Ser	Ser	Val	Thr	Leu	Ser	
					325					330					335	
CCT	CTT	CAT	TCC	CTA	CAA	TCT	CCT	CAC	ACC	TAT	GTT	TCC	CAC	ACC	ACA	1054
Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tyr	Val	Ser	Asp	Thr	Thr	
				340					345					350		
TCC	TCT	CCA	ATC	ATT	ACA	TCC	CCT	GGG	ATC	TTA	CAG	CCC	TCA	CCC	AAC	1102
Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu	Glu	Ala	Ser	Pro	Asn	
				355				360					365			
CCT	ATG	TTC	CCC	AGT	CCC	CCC	CCT	CCT	CCC	CCA	CTC	CAT	CCC	CAG	CAT	1150
Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Glu	His	
				370			375					380				
CCA	CTA	TCT	TTT	TCT	AAC	CTT	CAT	GAA	ATC	CAG	CCT	TTC	CCA	CAT	CCG	1198
Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Glu	Pro	Leu	Ala	His	Gly	
						390					395					
CCC	ACC	ACT	CTC	CTT	CCC	TCA	GTC	AGC	CAG	TTG	CTA	TCC	CAC	CAC	CAC	1246
Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Glu	Leu	Leu	Ser	His	His	His	
					405				410						415	
ATT	GTC	TCT	CCA	AGT	GGC	AGT	CCT	GCA	ACC	TTC	AGT	ACC	CTC	CAT		1294
Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	
				420				425					430			
CCA	GTC	CCA	GTC	CCA	CCA	CAT	TCC	ATC	AAC	CCC	ATC	CAG	GTC	AAT	CAC	1342
Pro	Val	Pro	Val	Pro	Ala	Asp	Tyr	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	
				435				440					445			
ACC	CAC	TAC	AAT	CAG	ATC	TTT	GCT	ATC	GTC	CTC	CCT	CCA	CCT	CAC	CCC	1390
Thr	Glu	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	
				450			455					460				
ACC	CAT	CCT	CCC	ATA	CCT	CCC	CAG	AGC	AGC	CCA	CCT	CAA	CCC	AAG	CAC	1438
Thr	His	Pro	Gly	Ile	Ala	Pro	Glu	Ser	Arg	Pro	Glu	Gly	Lys	His		
				465		470				475						
ATA	ACC	ACC	CCT	CCG	CAC	CCC	TTC	CCC	CCC	ATT	CTC	ACT	TTC	CAC	CTC	1486
Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Glu	Leu	
				485				490							495	
ATC	CCT	AAA	CCC	AGT	ATT	CCC	CAA	CCA	CCC	CCC	CCT	CCC	CAC	CCT	CAC	1534
Ile	Pro	Lys	Gly	Ser	Ile	Ala	Glu	Pro	Ala	Gly	Ala	Pro	Glu	Pro	Glu	
				500				505						510		
TCC	ACC	TCC	CCT	CCA	CCT	GTT	GGC	GGC	CCC	CTC	CCC	ACC	ATC	TAC	CAC	1582
Ser	Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Glu	
				515				520					525			
ATT	CCA	CAA	ATC	CCG	CCT	TTC	CCC	AGT	GTC	CCT	TTC	CCC	ACT	CCC	ATC	1630
Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	
				530			535					540				

Figure 11 Cont'D

ATC CCC CAG CAG CAG GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr 545 550 555	1678
CAT CCT TTC CCA GCC TCT CTC GGC AAC TAC CCC ACA CCC CCT TCA CAG Ile Phe Phe Phe Ala Ser Val Gly Tyr Tyr Pro Thr Pro Pro Ser Gln 560 565 570 575	1726
CAC AGT TAT GGT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT Ile Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser Ile Ser 580 585 590	1774
GGT CAC CTC CAG GGT CAG CAT CCC TAC CTC ACA CCA TCC CCA GAG TCT Gly Ile Leu Gln Gly Glu Ile Pro Tyr Leu Thr Pro Ser Pro Glu Ser 595 600 605	1822
CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro Ile Ser Ala Ser Asn Trp Ser 610 615 620	1870
CAT CTC ACC ACC ACC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CGG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Glu Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATC TCT GAG CCA CCA CAC AAC AAC ATC CAG GTT Gly Pro Gly Thr Ile Met Ser Glu Pro Pro Ile Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TCGACAGAGTC CACCTCCAGT GTAGAGACAT AACGACITTT TGTAAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTCG ACCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAAG TGTTCCTATT CAGATAATGC AAGAGAAAGCA ATTGCTCAGT	2142
TTCACTCGGT ATCTGCAGAG CTTATTCATT ATTCTAATCT AATAAGACAA GTTGTGGAA	2202
ATGCCAAGATC AATACAAAGCC TTGGGTCCAT GTTACTCTC TTCTATTTCG AGAATAAGAT	2262
GGATGCTTAT TGAAGCCGAG ACATTCTTGC AGCTTGGACT GCATTTTAAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATCAGAA GATTCTACAC TAGCGTCTCG TTGGGAATTA TCCCTCGAA	2382
TTCTGCCGCA ATTGACCTAC GCATCTCTCT CTCCTTGGAC ATTCTTTTGT GTTCAATTTGG	2442
TGCTTTTGGT TTTCACCTTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAGAC	2502
CTTTGTGCTT TTGATCATTC TGGCCCATCA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCCGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTCTCT AGCACAALACC	2622
TTTCAAGTAT GTTGTCTCT TGGAAAATGG ACATACTCTA TTGTGTCTCT CTGCATATAT	2682
CATTCTTCCA CACAGAAAGG GAGAAAGATA CTTTCTTCA ACAAATTTTC CCGGCAGGAG	2742
ATCCCTTCAA CAGGCTGCAC CTTAATTTTT CTGTCTCTCT TCCAGGTCTT CATATAAACT	2802
TTACCAGGAA GAAGGGTCTG AGTTTGTGT TTTTCTGTGT ATGGGCTCTG TCACTCTAAA	2862
GTTTTATCCT TCAATCTCTA GTTACTATGA CCGTCCCCAC TTTTTTAAAA CCAAGAAAAG	2922
GTTCGAATG TTGCAATGAC CAAAGAGACAA GTTAATCTGT CCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CTAATTCCT GCCAAGCATT CCAATGACTC CCTGTATGGA ACACATTTGT	3042
CCCAGATCTG AGCATTCCTG CCGTGTITTA CTCACTTACC CAGCATATGA AACATGCTT	3102
AACGTCTGAG CTTTTCTTT CATATCCACA GAAGAGACTG TCTCAAAATG TGTACCTTTC	3162

Figure 11 Cont'D

CCATTTAGCA CTGAACCTTC CTTAGCCCAA GGCACCCAGT GACAGTTCG TCCTGTTTGT	3222
CAGATGATCA GTCTCTACGC ATTATCTTGC TGCTTAAAGG CCCTGTCACC AATCTTTCTT	3282
TCACACCGTG TGGTCCGTGT TACTGCTATA CCCAGTATGT TCTGACTGAA GACATGGACT	3342
TATATGCTTC AAGTGCAGGA ATTGGAAGGT TGGAGTTCCT TCTATGATC CAAAACAGCC	3402
CTATAAGGAG GTTGCAGGAG GAGGAAGTAT ATAGCAGCGT TTGCTATTTT CTGCTACCAT	3462
TTCTTTTCTT CTGAAGCCGC CATGACATTC CCTTGGCCAA CTAAAGTAGA AACTCAACAG	3522
AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGGTCA	3582
TGTTTCAGAC TGATTGCCCC TCACCTGAAT CCAGTCTCTG TATTCAATCT CTGGCCAAAT	3642
TCTTTGACTT TCTTTTAAAG GCAGAAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT	3702
CTTCTCTTTC TCGTTGGGGC AGTTAATAAT TGGTCCATGC GTACAGTCCA ACCTCCGTCC	3762
AGTCTCTGTA TGGCCATGAC ACCTGCCAAA TAAGTTCTGC CTGGCCATTT TGTAGATAAT	3822
AACAGGTCAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCTTT CTATCCCTGC	3882
AAGTATGCAT CAGTGCCTCC CACTTACCTG ATTGTCTCTT CCGTGGCCCC ATATGGAAAC	3942
CGTCCGTCTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCTAT CCAAAATTTAT	4002
TGAACCAACA AAAATAATTA CTCTGCCCCT CAGATAAGCA GATTAAATTT GTTCATCTCT	4062
TGCTTAAATC TCTCCATGTG GCAACATTCT CTCAGCCTCT TTCAATAGGT GCAAAACATT	4122
TATCATTTCTA AATGGTGAAT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
ACCTATCTGC ATGGAGCCCTC ACCATCCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG	4242
GGGATGGCGA TCACTTTCTT CCCCTG	4268

Figure 12A

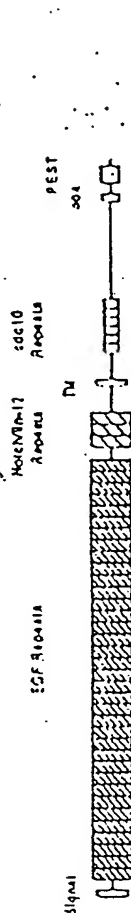


Figure 12A

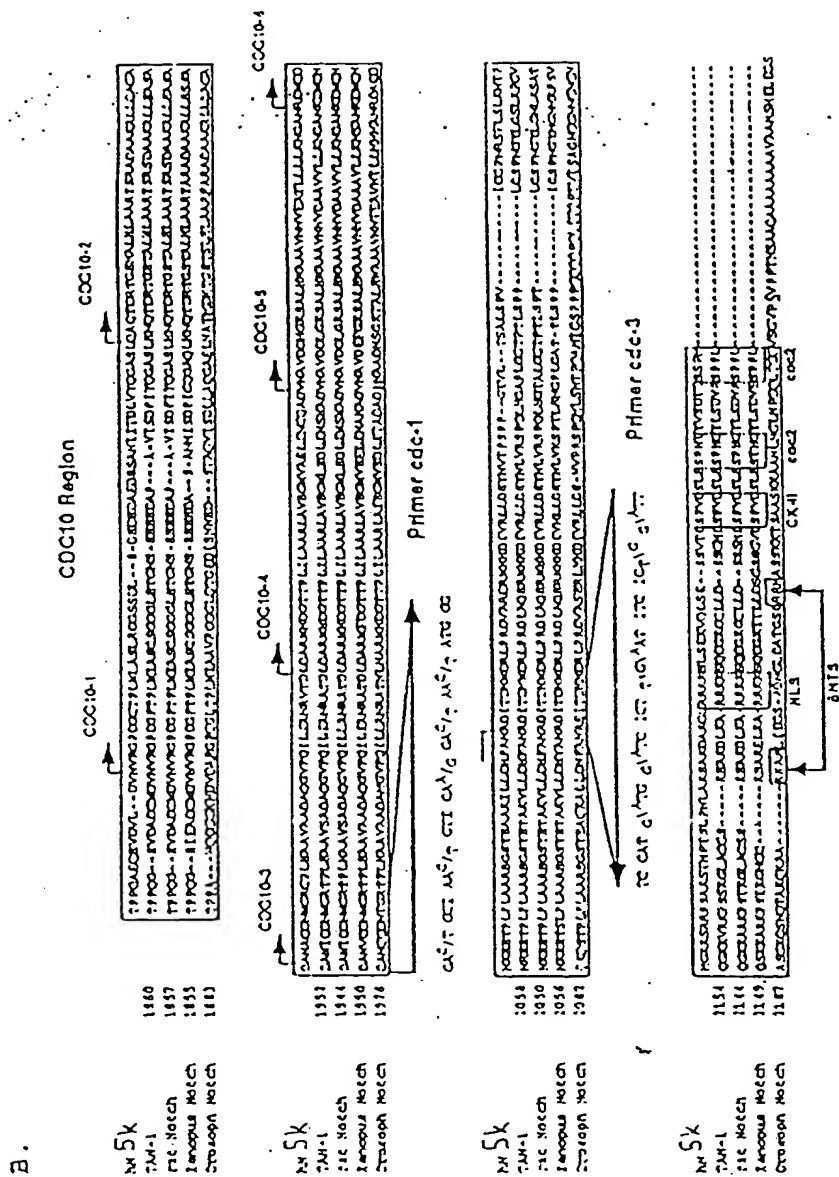


Figure 13

Potential signal cleavage site

EGF-like Repeats

HP-----ALRAL LVALALALAL CA-----APA HA-----GRGRTGECV NGRGRTGECV OTGYCKPQED FLADYCKQNR PCE-KNRCON GGTC--VAQA
 HP-----LAPILALAL PA-----LAA RG-----RCSPQETCL NGRGRTA-AN GTACVCGGA FVPRCPQPN PCL-STPCN AGTCVHDDR
 MD-----RIGLVAHCL NGRGRTCPN GTGCTGCLNH YTGCTGCLNH PCTTKNCHN FOTCEPVLQ
 HQ-----PASPULULUT LAFALHNLV RGTOTALVA SCTSVG--CQ NGOTGVLTQLN OKTYCACAOSH VYDYCEHRN PCN-SHRCN GGTCQVTRFQ
 HQ-----INKHIAVASL PASLULULUT LAFALHNLV RGTOTALVA SCTSVG--CQ NGOTGVLTQLN OKTYCACAOSH VYDYCEHRN PCN-SHRCN GGTCQVTRFQ

HLGNATCRCA SGTGTGDCQY STSHPCFYSR PCLNGGTGCHN LSRDT-VECT CQVGTGTAEC QMTDAGLSHP CANGSTCTTV --ANQFSCK LGTGTQACE TDWNEC-DTP CHCNGGCTCL
 GVADYACSCA LGTSGPULCT PLUNAC-LTN PCRGGTGCL LN-LTETXCR PGMWMSKSC QQAQACSLP --EASYICHC PPSFPHQPCR QDWECCQAP RLCRNGGTCN
 NAITDFICHP VGTGTNVLCT PVDNAC-VNN PCRGGTGCL LN-LTETXCR PGMWMSKSC QQAQACSLP --EAYICHC PPSFPHQPCR QDWECCQAP RLCRNGGTCN
 CHPLGCKCHP LGTDESLECI AVPMAC-DHV TCLNGGTGCL LN-LTETXCR PGMWMSKSC QQAQACSLP --EAYICHC PPSFPHQPCR QDWECCQAP RLCRNGGTCN

NLPFSYQCC PQGTGTQYCD SLVYPCASBP CVMGTGCRQT GDTFTGECNL PGTGTGTCR NIDDCPNHRC QNGQGVGVGV NTYNCRCPQP VTGQGTCTEDV DECLLQINA- CQNGGTGCHN
 NEVGSYACVC RATHGTQPNCE RLVYPCASBP CVMGTGCRQT GDTFTGECNL PGTGTGTCR NIDDCPNHRC QNGQGVGVGV NTYNCRCPQP VTGQGTCTEDV DECLLQINA- CQNGGTGCHN
 NEVGSYACVC RATHGTQPNCE RLVYPCASBP CVMGTGCRQT GDTFTGECNL PGTGTGTCR NIDDCPNHRC QNGQGVGVGV NTYNCRCPQP VTGQGTCTEDV DECLLQINA- CQNGGTGCHN
 NTHGYSYCHC PGTGTQYCD TKNYPCASBP CVMGTGCRQT GDTFTGECNL PGTGTGTCR NIDDCPNHRC QNGQGVGVGV NTYNCRCPQP VTGQGTCTEDV DECLLQINA- CQNGGTGCHN

NGGYGVGVV QHSGDQSEN IDDCAFACST PGSTGTORVA SFSCCHPEK AGLLCHLDDA CISPCHMGA LGDTNPLUKG YICTPQGYT QACTQEDVDE CAAHNSNCE HAGKCVNTQ
 HGTNVCVW QMTGDCSEN IDDCAFACST PGSTGTORVA SFSCCHPEK AGLLCHLDDA CISPCHMGA LGDTNPLUKG YICTPQGYT QACTQEDVDE CAAHNSNCE HAGKCVNTQ
 HGTNVCVW QMTGDCSEN IDDCAFACST PGSTGTORVA SFSCCHPEK AGLLCHLDDA CISPCHMGA LGDTNPLUKG YICTPQGYT QACTQEDVDE CAAHNSNCE HAGKCVNTQ
 HGTNVCVW QMTGDCSEN IDDCAFACST PGSTGTORVA SFSCCHPEK AGLLCHLDDA CISPCHMGA LGDTNPLUKG YICTPQGYT QACTQEDVDE CAAHNSNCE HAGKCVNTQ

AFHCEILKQV AGPRCEHDIN ECHSDPCQND ATCLQKIQSF TCLQMGFKVQ VHCLEINEC QSNPCVNGQ CVDKYNRFG LQPGTGTQV CQIDIDGSS TPKNGAKCI QHPNGYECQ
 STECCOQOY TQPRCEHDIN ECHSDPCQND ATCLQKIQSF TCLQMGFKVQ VHCLEINEC QSNPCVNGQ CVDKYNRFG LQPGTGTQV CQIDIDGSS TPKNGAKCI QHPNGYECQ
 STECCOQOY TQPRCEHDIN ECHSDPCQND ATCLQKIQSF TCLQMGFKVQ VHCLEINEC QSNPCVNGQ CVDKYNRFG LQPGTGTQV CQIDIDGSS TPKNGAKCI QHPNGYECQ
 STECCOQOY TQPRCEHDIN ECHSDPCQND ATCLQKIQSF TCLQMGFKVQ VHCLEINEC QSNPCVNGQ CVDKYNRFG LQPGTGTQV CQIDIDGSS TPKNGAKCI QHPNGYECQ

ATGFTVGLCE ENIDNCDP CHHQCQDGI DSYTCINRG YHQAICSDQI DECVSLPCLN DQRCIDLNVG YQNCQPPQS QVNCINFDQ CASNPGCH- ICHQDINRVS CVCSPFTQ
 TQVYTHACE VQDCECDP CHHQCQDGI DSYTCINRG YHQAICSDQI DECVSLPCLN DQRCIDLNVG YQNCQPPQS QVNCINFDQ CASNPGCH- ICHQDINRVS CVCSPFTQ
 TQVYTHACE VQDCECDP CHHQCQDGI DSYTCINRG YHQAICSDQI DECVSLPCLN DQRCIDLNVG YQNCQPPQS QVNCINFDQ CASNPGCH- ICHQDINRVS CVCSPFTQ
 TQVYTHACE VQDCECDP CHHQCQDGI DSYTCINRG YHQAICSDQI DECVSLPCLN DQRCIDLNVG YQNCQPPQS QVNCINFDQ CASNPGCH- ICHQDINRVS CVCSPFTQ

RCHIDIDCA SNPCRKATC INGVNGFACI CPEGPHHPS YSOVNECLN PCI-HNCTG GLSYGKCLD AGHGVNCEV DKNELSNPC QNGGTCDNLV NGYRTCTCKG FKYNHCQNI
 MCKSHIDCA SNPCRKATC INGVNGFACI CPEGPHHPS YSOVNECLN PCI-HNCTG GLSYGKCLD AGHGVNCEV DKNELSNPC QNGGTCDNLV NGYRTCTCKG FKYNHCQNI
 MCKSHIDCA SNPCRKATC INGVNGFACI CPEGPHHPS YSOVNECLN PCI-HNCTG GLSYGKCLD AGHGVNCEV DKNELSNPC QNGGTCDNLV NGYRTCTCKG FKYNHCQNI
 MCKSHIDCA SNPCRKATC INGVNGFACI CPEGPHHPS YSOVNECLN PCI-HNCTG GLSYGKCLD AGHGVNCEV DKNELSNPC QNGGTCDNLV NGYRTCTCKG FKYNHCQNI

OCASINCLN QGTCTDIDLG YTHCVLPYT GNGQCTVLAP CSPNCDMA VKESPNFES YTCCLCA-PQV QOQRTCTDID EC-LSKPNH- HCLCHNTQGS YHCECPPTS OHDCLEIDQ
 HECASINCLN QGTCTDIDLG YTHCVLPYT GNGQCTVLAP CSPNCDMA VKESPNFES YTCCLCA-PQV QOQRTCTDID EC-LSKPNH- HCLCHNTQGS YHCECPPTS OHDCLEIDQ
 HECASINCLN QGTCTDIDLG YTHCVLPYT GNGQCTVLAP CSPNCDMA VKESPNFES YTCCLCA-PQV QOQRTCTDID EC-LSKPNH- HCLCHNTQGS YHCECPPTS OHDCLEIDQ
 HECASINCLN QGTCTDIDLG YTHCVLPYT GNGQCTVLAP CSPNCDMA VKESPNFES YTCCLCA-PQV QOQRTCTDID EC-LSKPNH- HCLCHNTQGS YHCECPPTS OHDCLEIDQ

CLANPCQNG SCHDQVNTES CLCLPQFTQ KQGTORNECL SEPCKNGTC SDYVNSYCK CQAGFDVHC ENNINECTES SCNGQCTVD GINSFCLCP VGTGTGTCUL EINESSNPC
 CRPNPCQNG SCHDQVNTES CLCLPQFTQ KQGTORNECL SEPCKNGTC SDYVNSYCK CQAGFDVHC ENNINECTES SCNGQCTVD GINSFCLCP VGTGTGTCUL EINESSNPC
 CRPNPCQNG SCHDQVNTES CLCLPQFTQ KQGTORNECL SEPCKNGTC SDYVNSYCK CQAGFDVHC ENNINECTES SCNGQCTVD GINSFCLCP VGTGTGTCUL EINESSNPC
 CRPNPCQNG SCHDQVNTES CLCLPQFTQ KQGTORNECL SEPCKNGTC SDYVNSYCK CQAGFDVHC ENNINECTES SCNGQCTVD GINSFCLCP VGTGTGTCUL EINESSNPC

LMGTCTVDL GTYRSCPLG YTGNGCTVL NUCRSPOKH KQGTQKXAE SQGLCPQSA QAYGVDPHVS-CDIAASRRG LVHLCQHSO VCTMAGNTH COCPLOYTGS YCEOLOECA
 LMGTCTVDL GTYRSCPLG YTGNGCTVL NUCRSPOKH KQGTQKXAE SQGLCPQSA QAYGVDPHVS-CDIAASRRG LVHLCQHSO VCTMAGNTH COCPLOYTGS YCEOLOECA
 LMGTCTVDL GTYRSCPLG YTGNGCTVL NUCRSPOKH KQGTQKXAE SQGLCPQSA QAYGVDPHVS-CDIAASRRG LVHLCQHSO VCTMAGNTH COCPLOYTGS YCEOLOECA
 LMGTCTVDL GTYRSCPLG YTGNGCTVL NUCRSPOKH KQGTQKXAE SQGLCPQSA QAYGVDPHVS-CDIAASRRG LVHLCQHSO VCTMAGNTH COCPLOYTGS YCEOLOECA

Figure 13 Cont'D

hum N	1267	SNPQICATC SDIYGYRCE CVPYQYVNC EYEDQCHD PCQOCTCID LVNHKSCSP ROTGRLICEE NIDOCAR---	1271	YSCRLRGA GERCEODINE
TAN-1	1271	PSPCQATC TDYLYGYSCE CVAYOHVNC SEEDQCHD PCQOCTCID LVNHKSCSP ROTGRLICEE NIDOCAR---	1275	YSCRLRGA GERCEODINE
Xen N	1269	PNPCQATC TDYLYGYSCE CVAYOHVNC SEEDQCHD PCQOCTCID LVNHKSCSP ROTGRLICEE NIDOCAR---	1279	YSCRLRGA GERCEODINE
Dros N	1300	SPQOQATC RDLYGATCQ CROGQOQVNC EYEDQCHD PCQOCTCID LVNHKSCSP ROTGRLICEE NIDOCAR---	1304	YSCRLRGA GERCEODINE
hum H	1376	CLSNPCSDG SUDCIQTLND YLVCRSATF GRHCTEVDV CPHQCLNGO TCVAVSNPO GFICRCPPGF SOARQCS---	1380	GRICRCPPGF SOARQCS---
TAN-1	1379	CLSNPCDRO TONCVRVND FHCRCBAGT ORCESVING CKCKPCNGO TCVAVSNPO GFICRCPPGF SOARQCS---	1383	GRICRCPPGF SOARQCS---
Xen H	1387	CLSNPCSDG TONCVRVND FHCRCBAGT ORCESVING CKCKPCNGO TCVAVSNPO GFICRCPPGF SOARQCS---	1391	GRICRCPPGF SOARQCS---
Dros N	1415	CLSNPCSDG TONCVRVND FHCRCBAGT ORCESVING CKCKPCNGO TCVAVSNPO GFICRCPPGF SOARQCS---	1419	GRICRCPPGF SOARQCS---
hum H	1476	GC-ASSPCQ HGSCCHPQO PPTVSCQAP PFSGRCEI	1480	YTPAPP---
TAN-1	1501	SPC-ASHPCY NGCTCFQAE EPTGCFQK NFNGFCHL	1505	YTPAPP---
Xen N	1495	DEC-SPNCA QCAACEDLLG D--VECLCP	1509	YTPAPP---
Dros H	1531	DEC-SPNCA QCAACEDLLG D--VECLCP	1535	YTPAPP---
hum H	1591	NN-QDELCN TVECLTDFE CQNSKTKC	1595	YTPAPP---
TAN-1	1519	SDCHKSDCN SAGCLTDFE CQNSKTKC	1523	YTPAPP---
Xen N	1615	NOCKSDCN MTGCLYDGF CQNSKTKC	1619	YTPAPP---
Dros N	1650	NOCKSDCN MTGCLYDGF CQNSKTKC	1654	YTPAPP---
hum N	1690	YTGKSAH KQ--R-----	1694	YTPAPP---
TAN-1	1717	YTGKSAH KQ--R-----	1721	YTPAPP---
Xen N	1730	YTGKSAH KQ--R-----	1734	YTPAPP---
Dros H	1745	YTGKSAH KQ--R-----	1749	YTPAPP---
hum N	1792	CLAVAVIIL FILLQVTH	1796	YTPAPP---
TAN-1	1817	CLAVAVIIL FILLQVTH	1821	YTPAPP---
Xen N	1831	CLAVAVIIL FILLQVTH	1835	YTPAPP---
Dros N	1861	CLAVAVIIL FILLQVTH	1865	YTPAPP---
hum N	1902	PIDRRMTQO HLEAADIAT PSLATPPO	1906	YTPAPP---
TAN-1	1934	QTDHROMTQO HLEAADIAT PSLATPPO	1938	YTPAPP---
Xen H	1949	QTDHROMTQO HLEAADIAT PSLATPPO	1951	YTPAPP---
Dros H	1976	QTDHROMTQO HLEAADIAT PSLATPPO	1978	YTPAPP---
hum N	2022	ANQDNHRC PLHAAVAAD QOVQILIRN	2026	YTPAPP---
TAN-1	2074	ANQDNHRC PLHAAVAAD QOVQILIRN	2078	YTPAPP---
Xen N	2069	ANQDNHRC PLHAAVAAD QOVQILIRN	2071	YTPAPP---
Dros N	2096	ANQDNHRC PLHAAVAAD QOVQILIRN	2098	YTPAPP---
hum N	2127	YDAKILLOH FANROITDHH DRLEPRVAD	2131	YTPAPP---
TAN-1	2178	YDAKILLOH FANROITDHH DRLEPRVAD	2182	YTPAPP---
Xen H	2208	YDAKILLOH FANROITDHH DRLEPRVAD	2212	YTPAPP---
Dros N	2269	YDAKILLOH FANROITDHH DRLEPRVAD	2273	YTPAPP---
hum N	2313	YDAKILLOH FANROITDHH DRLEPRVAD	2317	YTPAPP---
TAN-1	2327	YDAKILLOH FANROITDHH DRLEPRVAD	2331	YTPAPP---
Xen N	2327	YDAKILLOH FANROITDHH DRLEPRVAD	2331	YTPAPP---
Dros N	2327	YDAKILLOH FANROITDHH DRLEPRVAD	2331	YTPAPP---

[illegible]

Figure 14

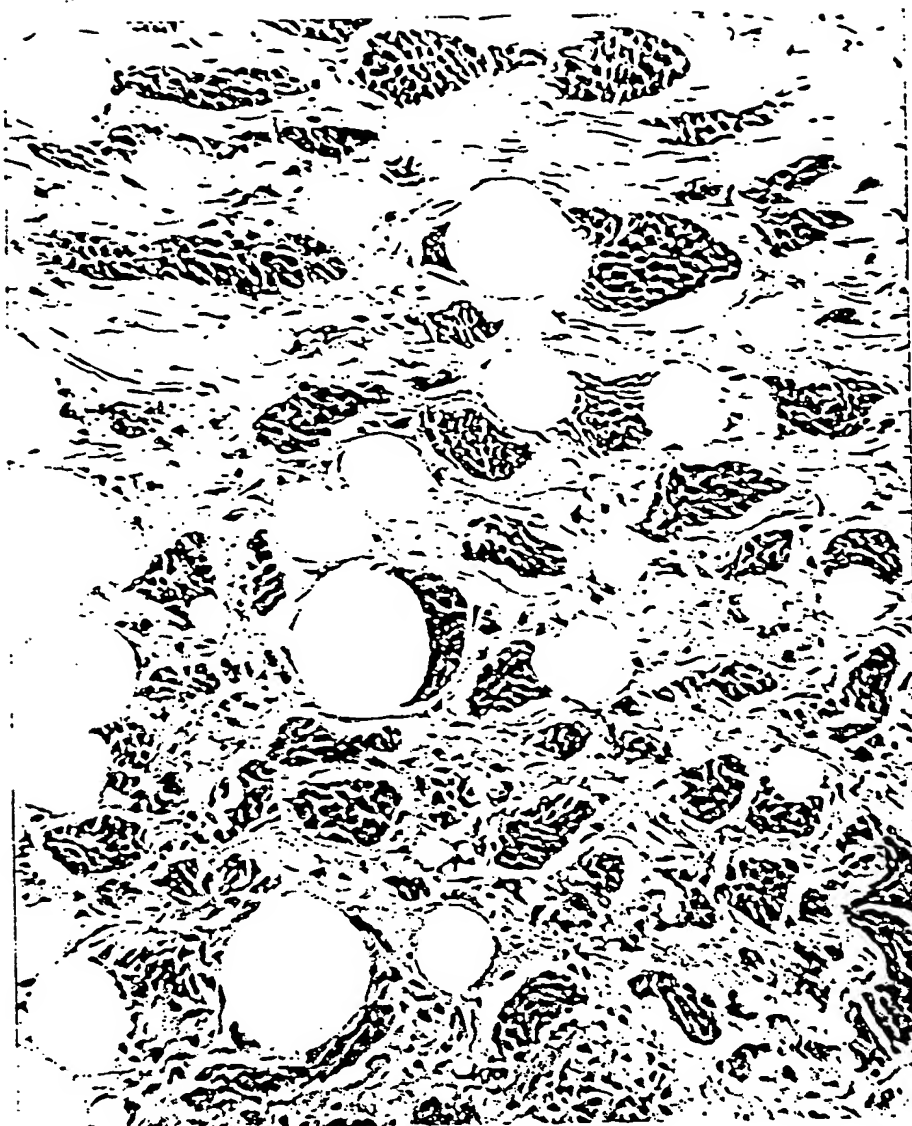


Figure 15A

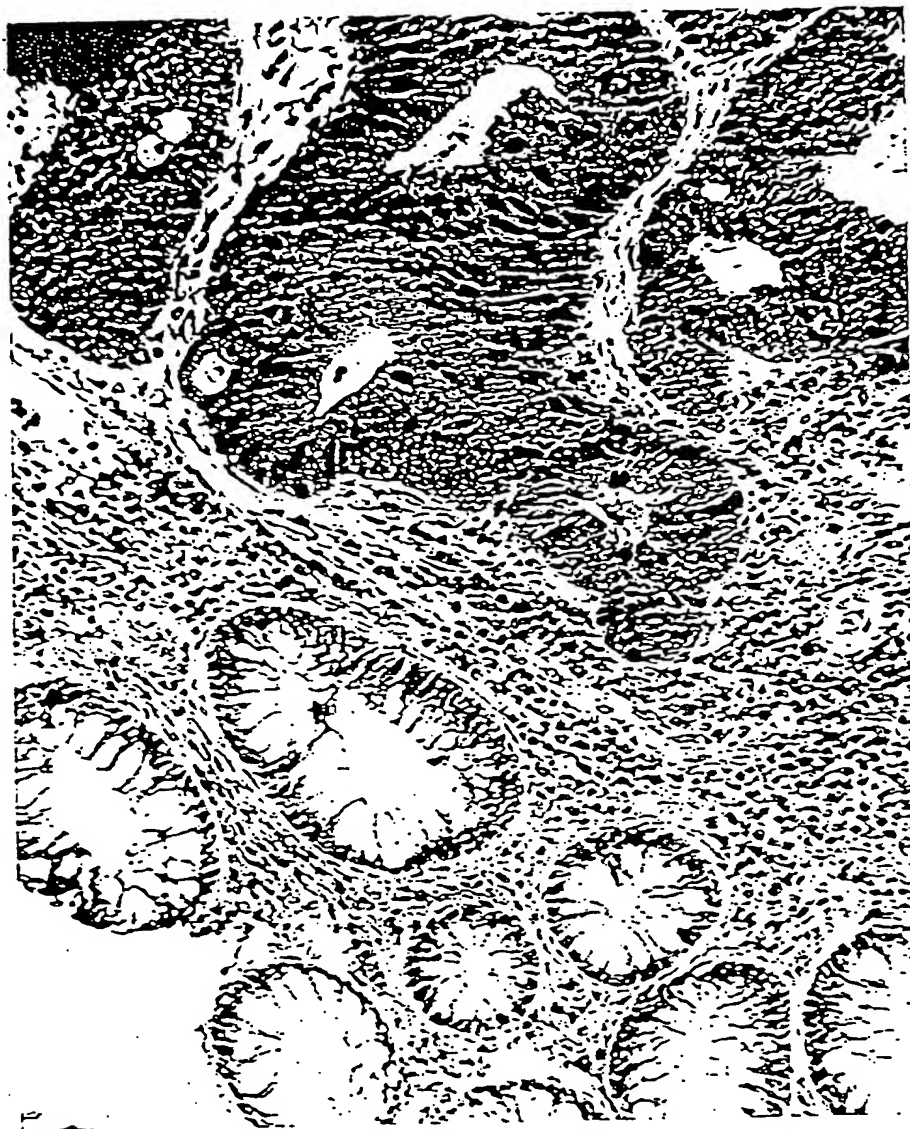


Figure 15B



Figure 16A



Figure 16B



Figure 17

10 * CGGCCCTGG CCCGCTCTG CTGTGGGCG TCGTGGGCT CTGGCTGTC TCGCGGGCC CGCGCATGC ATTGCAGTG
 P A L R P A L L W A L L A L W L C C A A P A B A L Q C>
 100 * ATGAACCTG TGTAAATGA GGAATGTG TTACTTACCA CAATGCACA GGAFACTGA AATGTCCAGA AGCTTCTTG
 R D G Y E P C V N E G M C V T Y H N G T G Y C K C P E G F L>
 190 * GTCAACATCG AGACCCCTGT GAGAGAACC GCTGCCAGAA TGGTGGGACT TGTGTGGCC AGGCCATGCT GGGGAAGCC
 G E Y C Q H R D P C E K N R C Q N G G T C V A Q A M L G K A>
 280 * GTGCTCAGG GTTTACAGGA GAGACTGCC AGTACTCAAC ATCTATCCA TGCTTGTGT CTGACCCCTG CCTEATGGC
 T C R C A S G F T G E D C Q Y S T S H P C F V S R P C L N G>
 370 * ATATGCTCAG CCGGATACC TATGAGTGA CCTGTCAAGT CCGGTTTACA GGTAAAGAGT GCCAATGGAC GGATGCTGC
 G T C H M L S R D T Y E C T C Q V G F T G K E C Q W T D A C>
 460 * CCTGTGCATA TGGAAATACC TGTACCACTG TGGCCAACA GTTCTCTGCA AATGCTTCA CAGCTTAC AGGGCAGAA
 L S H P C A N G S T C T T V A N Q F S C K C L T G F T G Q K>
 550 * ATGTCAATGA GTGTGACATT CCAGGACACT GCCAGCATGG TGGCAGCTGC CTCACCTGC CTGGTTCCTA CCAGTGGCAG
 C E T D V N E C D I P G H C Q H G G T C L N L P G S Y Q C Q>
 640 * GCTTCACAGG CCAGTACTGT GACAGCTGT ATGTGCCCTG TGCACCTCA CCTTGTGTC AATGAGGCAC CTGTGGCAG
 C P Q G F T G Q Y C D S L Y V P C A P S P C V N G G T C R Q>
 730 * GTGCACTGC CTTCAGGTT TTGAAGGAG CACCTGTGAG AGGAATATTG ATGACTGCC TTACCACAGG
 T G D F T F E C N C L P G F E G S T C E R N I D D C P N H R>

Figure 17 Cont'D

820 * 830 * 840 * 850 * 860 * 870 * 880 * 890 * 900 *
 TGTGAGATG GAGGGTTTG TGTGGATGG GTCAACATTT ACAACTGCGG CTGTCCGCCA CAATGACAG GACAGTTCTG CACAGAGAT
 C Q N G G V C V D G V N T Y N C R C P P Q W T G Q F C T E D>

 910 * 920 * 930 * 940 * 950 * 960 * 970 * 980 * 990 *
 GTGATGAAT CCTGCTGCA GCGCAATGCC TGTCAAAATG GGGGACCTG TGGCAACCGC AATGAGGCT ATGGCTGTGT ATGTGTCAAC
 V D E C L L Q P N A C Q N G G T C A N R N G G Y G C V C V N>

 1000 * 1010 * 1020 * 1030 * 1040 * 1050 * 1060 * 1070 * 1080 *
 GGCTGGAGTG GAGATGACTG CAGTGAGAAC ATGTGATGTT GTGCTTCCG CTCTGTACT CCAGGCTCCA CCTGCATCGA CCGTGTGCC
 G W S G D D C S E N I D D C A F A S C T P G S T C I D R V A>

 1090 * 1100 * 1110 * 1120 * 1130 * 1140 * 1150 * 1160 * 1170 *
 TCCCTCTCTT GCATGTGCC AGAGGGGAG GCAGGCTCTCC TGTGTCATCT GGATGATGCA TGCATCAGCA ATCCTTGCCA CAAAGGGGCA
 S F S C M C P E G K A G L L C H L D D A C I S N P C H K G A>

 1180 * 1190 * 1200 * 1210 * 1220 * 1230 * 1240 * 1250 * 1260 *
 CTGTGTGACA CCAACCCCT AAATGGCAA TATATTGCA CCTGCCACA AGCCTACAAA GGGGCTGACT GCACAGAAGA TGTGATGAA
 L C D T N P L N G Q Y I C T C P Q G Y K G A D C T E D V D E>

 1270 * 1280 * 1290 * 1300 * 1310 * 1320 * 1330 * 1340 * 1350 *
 TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGGAA AATGTGAA CACGGATGG GCCTTCCACT GTGAGTCTCT GAAGGTTAT
 C A M A N S N P C E H A G K C V N T D G A F H C E C L K G Y>

 1360 * 1370 * 1380 * 1390 * 1400 * 1410 * 1420 * 1430 * 1440 *
 GCAGGACCTC GTGTGAGAT GCACATCAAT GAGTCCCAT GAGTCCCAT CAGACCCCTG CCAGATGAT GCTACCTGTC TGGATAAGAT TGGAGCCTTC
 A G P R C E M D I N E C H S D P C Q N D A T C L D K I G G F>

 1450 * 1460 * 1470 * 1480 * 1490 * 1500 * 1510 * 1520 * 1530 *
 ACATGCTGT GCATGCCAGG TTTCAAGGT GTGATTTG AATTAGAAAT AATGAATGT CAGAGCAACC CTTGTGTGAA CAATGGCAG
 T C L C M P G F K G V H C E L E I N E C Q S N P C V N N G Q>

 1540 * 1550 * 1560 * 1570 * 1580 * 1590 * 1600 * 1610 * 1620 *
 TGTGTGATA AAGTCAATCG TTTCCAGTGC CTGTGCTCTC CTGTTTCCAGT TGGGCCAGTT TGGCAGATTG ATATTGATGA CTGTTCCAGT
 C V D K V N R F Q C L C P P G F T G P V C Q I D I D C S S>

Figure 17 Cont'D

1630	1640	1650	1660	1670	1680	1690	1700	1710
ACTCCGTGTC	TGRATGGGC	AAAGTGTATC	GATCACCAG	ATGCTATCA	ATGCCAGTT	ATCCAGTT	ATCAGTGT	GTGTGTGAG
T P C	L N G A	K C I D	H P N G	Y E C Q	C A T G	F T G V	L C E	
1720	1730	1740	1750	1760	1770	1780	1790	1800
GAGAACATTG	ACAACTGCA	CCCGATCCT	TGCCACCATG	GTCAGTGTCA	GGATGTTATT	GATTCATACA	CCTGCATCTG	CAATCCGGG
E N I	D N C D	P D P C	H G Q C	Q D G I	D S Y T	C I C N	P G	
1810	1820	1830	1840	1850	1860	1870	1880	1890
TACATGGCG	CCATCTGCAG	TGACCAGATT	GATGAAGTT	ACAGCAGCC	TTGCCCTGAC	GATGGTGGCT	GCATGACCT	GGTCAATGGC
Y M G	A I C S	D Q I D	E C Y S	S P C L	N D G R	C I D L	V N G	
1900	1910	1920	1930	1940	1950	1960	1970	1980
TACCAGTGCA	ACTGCCAGCC	AGGCACGTCA	GGGGTTAATT	GTGAATTAA	TTTGTATGAC	TGTGCAAGTA	ACCCTTGTAT	CCATGGAATC
Y Q C	N C Q P	G T S G	V N C E	I N F D	C A S N	P C I H	G I	
1990	2000	2010	2020	2030	2040	2050	2060	2070
TGATGATG	GCATTAAATCG	CTACAGTTGT	GTCTGCTCAC	CAGGATTCAC	AGGCACAGA	TGTAAATTTG	ACATTGATGA	GTGTGCTTCC
C M D	G I N R	Y S C V	C S P G	F T G Q	R C N I	D I D E	C A S	
2080	2090	2100	2110	2120	2130	2140	2150	2160
AAATCCCTGTC	GCAAGGTGC	AACATGTATC	AACGGTGTGA	ATGGTTCCG	CTGTATATGC	CCCGAGGAC	CCCATCACCC	CACCTGCTAC
N P C	R K G A	T C I N	G V N G	F R C I	C P E G	P H P S	C Y	
2170	2180	2190	2200	2210	2220	2230	2240	2250
TCAACAGTGA	ACGAATGCT	GAGCAATCCC	TGCATCCATG	GAACTGTAC	TGGAGTCTC	AGTGCATATA	ACTGTCTCTG	TGATCCAGGC
S Q V	N E C L	S N P C	I H G N	C T G G	L S G Y	K C L C	D A G	
2260	2270	2280	2290	2300	2310	2320	2330	2340
TGGGTTGGCA	TCAACTGTGA	AGTGCACAAA	AATGAATGCC	TTTCGATCC	ATGCCAGAT	GGAGGAATTT	GTGACATCT	GGTGAATGGA
W V G	I N C E	V D K N	E C L S	N P C Q	N G T C	D N L V	N G	
2350	2360	2370	2380	2390	2400	2410	2420	2430
TACAGGTGTA	CTTGCAAGAA	GGGCTTTAAA	GGCTATACT	GCAGGTGAA	TATTGATGAA	TGTGCTCTCAA	ATCCATGCT	GAACCAAGGA
Y R C	T C K F	G F K G	Y N C Q	V N I D	E C A S	N P C L	N Q	
2440	2450	2460	2470	2480	2490	2500	2510	2520

Figure 17 Cont'D

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*
ACCTGCTTTG ATGACATAAG TGGTACACT TGGCAGCTGT TGCTGCCATA CACAGGCAAG AATTGTCAGA CAGTATTGGC TCCCTGTTC
T C F D D I S G Y T C H C V L P Y T G X N C Q T V L A P C S>
2530
*
CCAAACCCCTT GTGAGATGC TGCTGTTTGC AAGAGTCAC CAATTTTGA GAGTTATCT TCGTTGTGTG CTCCTGGCTG GCAAGGTACAG
P N P C E N A A V C K E S P N F E S Y T C L C A P G W Q G Q>
2620
*
CGGTGTACCA TTGACATTGA CGAGTGTATC TCCAAGCCCT GCATGAACCA TGGTCTCTGC CATACACCCC AGGGCAGCTA CATGTGTGAA
R C T I D I D E C I S K P C M N H G L C H N T Q G S Y M C E>
2710
*
TGCCACCAG GCTTCAGTGG TATGACACTT GAGGAGACA TTGATCACTG CCTTGCACAT CCTTGCACGA ATGAGGCTTC CTGTATGGAT
C P P G F S G M D C E E D I D D C L A N P C Q N G G S C M D>
2800
*
GGAGTGATA CTTTCTCCTG CCTCTGCCCT CCGGGTTTCA CTGGGATAA GTGCCAGACA GACATGAATG AGTGTCTGAG TGAACCCCTGT
G V N T F S C L C L P G F T G D K C Q T D M N E C L S E P C>
2890
*
AAGAATGGAG GGACCTGCTC TGACTACGTC AACAGTTACA CTTGCAAGTG CCAGGCAGGA TTGTATGAG TCCATTGTGA GAACACATC
K N G G T C S D Y V N S Y T C K C Q A G F D G V H C E N N I>
2980
*
AATGAGTCCA CTGAGAGCTC CTGTTTCAAT GGTGGCAGAT GTGTTGATGG GATTAACCTC TTCTCTTCTT TGTGCCCTGT GGGTTTCACT
N E C T E S S C F N G G T C V D G I N S F S C L C P V G F T>
3070
*
GGATCCTTCT GCCTCCATGA GATCAATGAA TGCAGCTCTC ATCCATGCTT GAATCAGGGA ACGTGTGTG ATGGCCTGGG TACCTACCGG
G S F C L H E I N E C S S H P C L N E G T C V D G L G T Y R>
3160
*
TGCAGCTGCC CCTGGGCTA CACTGGGAAA AACTGTGAGA CCGTGGTGA TCTCTGCACT CGGTCTCCAT GTAAAACAA AGGTACTTGT
C S C P L G Y T G K N C Q T L V N L C S R S P C K N K G T C>
3250
*

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Figure 17 Cont'D

GTTCAGAAAA AAGCAGAGTC CCAGTGCCTA TGTCCATCTG GATGGCTG TGCCTATTGT GAGGTGCCCA ATGCTCTCTG TGACATAGCA
 V Q K K A E S Q C L C P S G W A G A Y C D V P N V S C D I A>
 3340 3350 3360 3370 3380 3390 3400 3410 3420
 GCGTCCAGGA GAGGTGCT TGTGAACAC TTGTGCCAGC ACTCAGGTGT CTGCATCAAT GGTGGCAACA CGCATTAAGT TCAGTCCGCC
 A S R R G V L V E H L C Q H S G V C I N A G N T H Y C Q C P>
 3430 3440 3450 3460 3470 3480 3490 3500 3510
 CTGGGCTATA CTGGGAGCTA CTGTGAGCAG CAACTCGATG AGTGTGGTGC CAACCCCTGC CAGCAGGGG CAACATGCAG TGACTTCATT
 L G Y T G S Y C E E Q L D E C A S N P C Q H G A T C S D F I>
 3520 3530 3540 3550 3560 3570 3580 3590 3600
 GGTGGATACA GATGGAGTGT TGTCCAGGC TATCAGGGTG TCAACTGCA GTATGAAGTG GATGAGTGC AGAATCAGCC CTGCCAGAAAT
 G G Y R C E C V P G Y Q G V N C E Y E V D E C Q N Q P C Q N>
 3610 3620 3630 3640 3650 3660 3670 3680 3690
 GGAGGCACCT GTATTGACCT TGTGAACAT TTCAAGTGTCT CTGCCCAGC AGGCACCTCG GGCCTACTCT GTGAAGAGAA CATTCATGAC
 G G T C I D L V N H F K C S C P P G T R G L L C E N I D D>
 3700 3710 3720 3730 3740 3750 3760 3770 3780
 TGTGCCGGG GTCCCATTTG CCTTAATGCT GGTCAAGTCA TGAATAGAT TGAGGGCTAC AGTTGTGCT GCTTGCCTGG CTTTGTCTGG
 C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G>
 3790 3800 3810 3820 3830 3840 3850 3860 3870
 GAGCGTTGTG AGGAGACAT CAACGAGTGC CTCTCCAGC CCTGCAGCTC TGAGGGCAGC CTGGACTGTA TACAGCTCAC CAATGACTAC
 E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y>
 3880 3890 3900 3910 3920 3930 3940 3950 3960
 CTGTGTGTTT GCCGTAGTGC CTTTACTGGC CGGCACCTGT AAACCTTCGT CGATGTGTGT CCGCAGATGC CCGCTCTGAA TGGAGGGACT
 L C V C R S A F T G R H C E T F V D V C P Q M P C L N G G T>
 3970 3980 3990 4000 4010 4020 4030 4040 4050
 TGTGTGTGG CCAGTAACAT GCCTGATGTT TTTATTTGCC GTTGTCCGCC GGAATTTCC GGGCAAGGT GCCAGAGCAG CTGTGACAAA
 C A V A S N M P D G F I C R C P P G F S G A R C Q S S C G Q>
 4060 4070 4080 4090 4100 4110 4120 4130 4140
 GTGAATGTA GGAAGGGGA GCAGTGTGTG CACACGGCCT CTGACCCCG CTTCTTCTGC CCCAGTCCC GGAAGTCCGA GTGAGGTGT

Figure 17 Cont'D

V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G C>
 4150 * 4160 * 4170 * 4180 * 4190 * 4200 * 4210 * 4220 * 4230 *
 GCAGTAGCC CCTGCCAGCA CGGGGGCACC TGCACCCCTC AGCGCAGCC TCCTATTAC TCCTGCCAGT GTGCCCCACC ATTCTGGGT
 A S S P C Q H G G S C B P Q R Q P P Y Y S C Q C A P P F S G>
 4240 * 4250 * 4260 * 4270 * 4280 * 4290 * 4300 * 4310 * 4320 *
 AGCGCTGT AACTCTAC GGCACCCCC AGCACCCCTC CTGCACCTG TCTGAGCCAG TATGTGCGG ACAAGCTCG GGATGCCGTC
 S R C E L Y T A P P S T P P A T C L S Q Y C A D K A R D G V>
 4330 * 4340 * 4350 * 4360 * 4370 * 4380 * 4390 * 4400 * 4410 *
 TGTGATGAG CCTGCAACAG CCATGCCCTG CAGTGGATG GGGTGACTG TTCTCTCACC ATGAGAACCC CTGGGCCAA CTGCTCTCTCC
 C D E A C N S H A C Q W D G G D C S L T M E N P W A N C S S>
 4420 * 4430 * 4440 * 4450 * 4460 * 4470 * 4480 * 4490 * 4500 *
 CCAGTCCCT CTTGGGATTA TATCAACAC CAGTGTGATG AGCTGTCAA CAGGTGCGAG TGCCTGTTG ACACTTTGA ATGCCAGGG
 P L P C W D Y I N N Q C D E L C N T V E C L F D N F E C Q G>
 4510 * 4520 * 4530 * 4540 * 4550 * 4560 * 4570 * 4580 * 4590 *
 AACAGCAAGA CATGCAAGTA TGACAATAC TGTGAGACC ACTTCAAGA CAACCACTGT AACGAGGGT GCAACACTGA GGAGTGTGT
 N S K T C K Y D K Y C A D H F K D N H C N Q G C N S E E C G>
 4600 * 4610 * 4620 * 4630 * 4640 * 4650 * 4660 * 4670 * 4680 *
 TGGATGGC TGGACTGTC TGCTGACCA CCTGAGACC TGGCAGAGG TACCCTGTT ATTGTGTTT TGATGCCACC TGAACAACCTG
 W D G L D C A A D Q P E N L A E G T L V I V V L M P P E Q L>
 4690 * 4700 * 4710 * 4720 * 4730 * 4740 * 4750 * 4760 * 4770 *
 CTCAGGATG CTCGAGCTT CTTCGGGCA CTGGGTACC TGTCTCACAC CAACCTGCGC ATTAGCGCG ACTGCCAGG GGAACCTATG
 L Q D A R S F L R A L G T L L H T N L R I K R D S Q G E L M>
 4780 * 4790 * 4800 * 4810 * 4820 * 4830 * 4840 * 4850 * 4860 *
 GTGTACCCCT ATTATGGTGA GAAGTCAGT GCTATGAAGA AACAGAGGAT GACAGCAGA TCCCTTCCTG GTGAACAAGA ACAGGAGTG
 V Y P Y Y G E K S A A M K K Q R M T R R S L P G E Q E Q E V>
 4870 * 4880 * 4890 * 4900 * 4910 * 4920 * 4930 * 4940 * 4950 *
 GCGAGTATA AGTCTTCTT GGAATATGAC AACCGACAGT GTGTCAAGA CTCAGACAC TCTTCAAGA ACACGAGGC AGCAGCACT
 A G S X V F L R I D N R Q C V Q D S G H C F K N T D A A A A>

Figure 17 Cont'D

4960 * CTCCTGGCCT CTCACGGCCAT ACAGGGACC CTTGTCATACC CTTCTTGTC TCCTGTCAGT GAATCCCTGA CTCACAGACG CACTCAGCTC
 L L A S H A I Q G T L S Y P L V S V V S E S L T P E R T Q L>
 5050 * CTCATCTCC TTGCTGTGC TGTGTGATC ATTCTGTTA TTATCTGCT GGGGTATC ATGCCAATC GAAGCGTAA GCATGCTCT
 L Y L L A V A V V I I L F I I L L G V I M A K R K R K H G S>
 5140 * CTCGGCTGC CTGAAGTTT CACTCTCC CGAGATGCAA GCATCACA GGTCTGTCAG CCAGTGGAC AGCATGCTGT GGGCTGAAA
 L W L P E G F T L R R D A S N H K R R E P V G Q D A V G L K>
 5230 * AATCTCTCAG TGCAGTCTC AGAAGCTAAC CTAACTGTA CTGGAACAAG TGAACACTGG GTGATGATG AAGGGCCCA GCCAAGAAA
 N L S V Q V S E A N L I G T G T S E H W V D D E G P Q P K K>
 5320 * GTAAGGCTG AAGATGAGC CTACTCTCA GAAGATG ACCCATGTA TCGACGGCA TGGACACAGC AGCAGCTTGA AGTTCAGAC
 V K A E D E A L L S E E D D P I D R R P W T Q Q H L E A A D>
 5410 * ATCCGTAGGA CACCATCGCT GGCTCTCACC CTTCTCAGG CAGACAGGA GGTGATGTTG TTAGATGTA ATGTCGTGG CCCAGATGGC
 I R R T P S L A L T P P Q A E Q E V D V L D V N V R G P D G>
 5500 * TGCACCCCAT TGATGTGGC TTCTCTCGA GGAGGCAGCT CAGATTGAG TGATCAAGAT GAAGATCAG AGCAGCTTTC TGCTACATC
 C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I>
 5590 * ATCAGACT TGGTCTACCA GGTGTCAGC CTCAGGCC CACAGACAGC GACTGTGAG ATGCCCTGC ACCTTCAGC CCGCTACTCA
 I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S>
 5680 * CCGGCTGATG CTCACAGCG TCTCTGGAT GCAGGTGAG ATGCCATGC CCAGACAAC ATGGGCGGT GTCCACTCCA TGCTGAGTG
 R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V>

Figure 17 Cont'D

5770	5780	5790	5800	5810	5820	5830	5840	5850
GCAGCTGATG CCCAAGCTGT CTTCAGATT CTGATTCGCA ACCGAGTAAC TGATCTAGAT GCAGGATGA ATGATGGTAC TACACCCCTG								
A A D A Q G V F Q I L I R N R V T D L D A R M N D G T T P L>								
5860	5870	5880	5890	5900	5910	5920	5930	5940
ATCTGGCTG CCGCCCTGGC TGTGAGGGA ATGTTGGAG AACTGATCAA CTGCCAAGC GATGTGATG CAGTGGATGA CCATGGARAA								
I L A A R L A V E G M V A E L I N C Q A D V N A V D D H G K>								
5950	5960	5970	5980	5990	6000	6010	6020	6030
TCGTCTCTC ACTGGGACG TGCTGTCAAT ATGTGGAGG CAACTCTTT GTTGTGAAA ATCGGGCCA ACCGAGAT GCAGGACAAC								
S A L H W A A A V N N V E A T L L L L K N G A N R D M Q D N>								
6040	6050	6060	6070	6080	6090	6100	6110	6120
AAGGAGAGA CACCTCTGTT TCTTGCTGCC CCGGAGGGA GCTATGAGC AGCCAAGTC CTGTAGACC ATTTGCCAA TCGAGACATC								
K E E T P L F L A A R E G S Y E A A K I L L D H F A N R D I>								
6130	6140	6150	6160	6170	6180	6190	6200	6210
ACAGACATA TGGATGCTT TCCCGGGAT GTGGCTGGG ATCCATGCA CCATGACAT ATCGGCTTC TGGATGATA CAATGACCC								
T D H M D R L P R D V A R D R M H H D I V R L L D E Y N V T>								
6220	6230	6240	6250	6260	6270	6280	6290	6300
CCAAGCCTC CAGGACCGT GTTCACTCT GCTCTCTAC CTGTATCTG TGGGCCCAAC AGATCTTTC TCAGCTGAA GCACACCCA								
P S P P G T V L T S A L S P V I C G P N R S F L S L K H T P>								
6310	6320	6330	6340	6350	6360	6370	6380	6390
ATGGGCAAGA AGTCTAGCG GCGCAGTGC AAGAGTACCA TGCTTACTAG CCTCCCTAAC CTTCGCAAG AGGCAAGGA TCCCAAGGT								
M G K K S R R P S A K S T M P T S L P N L A X E A K D A K G>								
6400	6410	6420	6430	6440	6450	6460	6470	6480
AGTAGGAGGA AGAAGTCTCT GAGTGAGAG GTCCAACTGT CTGAGAGTTC AGTAACTTA TCCCTGTG ATTCCCTAGA ATCTCTCAC								
S R R K K S L S E K V Q L S E S S V T L S P V D S L E S P H>								
6490	6500	6510	6520	6530	6540	6550	6560	6570
ACGTATGTT CCGACACAC ATCTCTCCA ATGATTACAT CCGCTGGAT CTTACAGGC CTTACCCACC CTATGTTGCC CACTGCCGCC								
T Y V S D T T S S P M I T S P G I L Q A S P N P M L A T A A>								
6580	6590	6600	6610	6620	6630	6640	6650	6660

Figure 17 Cont'D

CCCTCTGCC	CAGTCCATGC	CCAGCATGA	CTATCTTTT	CTAATCTCA	TGAATGCAG	CCTTGGCAC	ATGGGGCCAG	CACCTGCTT	*
P P A	P V H A	Q H A	L S F	S N L H	E M O	P L A	H G A S	T V L>	*
6670	6680	6690	6700	6710	6720	6730	6740	6750	*
CCCTCAGTGA	GCAGTGTCT	ATCCACACAC	CACATTTGT	CTCCAGCAG	TGGCAGTCT	GGACCTTCA	GTAGGCTCCA	TCCAGTCCA	*
P S V	S Q L L	S H H	H I V	S P G S	G S A	G S L	S R L H	P V P>	*
6760	6770	6780	6790	6800	6810	6820	6830	6840	*
GTCCACGAC	ATGGATGAA	CCGCATGGAG	GTGATGAGA	CCAGTACAA	TGAGATGTT	GGTATGGTCC	TGGCTCCAGC	TGAGGGCACC	*
V P A	D W M N	R M E	V N E	T Q Y N	E M F	G M V	L A P A	E G T>	*
6850	6860	6870	6880	6890	6900	6910	6920	6930	*
CATCTGGCA	TAGCTCCCA	GAGCAGCCA	CCTGAAGCA	AGCACATAC	CACCCCTCG	GAGCCCTGC	CCCCATTTT	GACTTCCAG	*
H P G	I A P Q	S R P	P E G	K H I T	T P R	E P L	P P I V	T F Q>	*
6940	6950	6960	6970	6980	6990	7000	7010	7020	*
CTATCCCTA	AAGCAGTAT	TGCCCCACCA	CGGGGGCTC	CCAGCCTCA	GTCCACCTGC	CCTCCAGCTG	TGCGGGGCC	CCTGCCACC	*
L I P	K G S I	A Q P	A G A	P Q P Q	S T C	P P A	V A G P	L P T>	*
7030	7040	7050	7060	7070	7080	7090	7100	7110	*
ATGTACAGA	TTCAGAAAT	GGCCCGTTG	CCCAGTGTG	CTTCCCCAC	TGCCATGATG	CCCCAGCAG	ACGGCAGGT	AGCTCAGACC	*
M Y Q	I P E M	A R L	P S V	A F P T	A M M	P Q Q	D G Q V	A Q T>	*
7120	7130	7140	7150	7160	7170	7180	7190	7200	*
ATTCTCCAG	CCTATCATCC	TTTCCCGCC	TCTGTGGCA	AGTACCCAC	ACCCCTTCA	CAGCACAGTT	ATGCTTCTC	AAATGCTGCT	*
I L P	A Y H P	F P A	S V G	K Y P T	P P S	Q H S	Y A S S	N A A>	*
7210	7220	7230	7240	7250	7260	7270	7280	7290	*
GAGGACAC	CCAGTCACAG	TGGTCACCTC	CAGGGTGAGC	ATCCCTACCT	GACACATCC	CCAGAGTCTC	CTGACCACTG	GTCAAGTTCA	*
E R T	P S H S	G H L	Q G E	H P Y L	T P S	P E S	P D Q W	S S S>	*
7300	7310	7320	7330	7340	7350	7360	7370	7380	*
TCACCCACT	CTGCTTCTGA	CTGTACAGAT	GTACACCACA	GGCCTACCCC	TGGGGTGTCT	GGAGGAGTCT	ACGGGGGACC	TGGGACACAC	*
S P B	S A S D	W S D	V T T	S P T P	G G A	G G G	Q R G P	G T H>	*
7390	7400	7410	7420	7430	7440	7450	7460	7470	*

[illegible]

Figure 17 Cont'D

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8470	8480	8490	8500	8510	8520	8530	8540	8550
CATTGACTGC	CTGATATGGAA	CACATTTC	CCAGATCTGA	GCATTCTAGG	CCCTGTTTAC	TCACTCACCC	AGCATATGAA	ACTAGTCTTA
8560	8570	8580	8590	8600	8610	8620	8630	8640
ACTGTGAGC	CTTTCCTTTC	ATATCCACAG	AAAGACACTGT	CTCAATGTT	GTACCCCTGC	CANTTAGSAC	TGAACITTC	TTAGCCCAAG
8650	8660	8670	8680	8690	8700	8710	8720	8730
GGACCCAGTG	ACAGTTGCT	TCCGTTTGC	AGATGATCAG	TCTCTACTGA	TTATCTTGCT	GCCTTAAGGC	CTGCTCACCA	ATCTTCTTT
8740	8750	8760	8770	8780	8790	8800	8810	8820
CACACCGTGT	GGTCCGNGTT	ACTGCTATAC	CCAGTATGTT	CTCAGTGAAG	ACATCGACTT	TATATGTTCA	AGTGCAGCAA	TTGGAAGTT
8830	8840	8850	8860	8870	8880	8890	8900	8910
GGACTTGTTT	TCTATGATCC	AAACAGCCC	TATAAGAAG	TTGGAAAGG	AGGAAGTATA	TAGCAGCCCT	TGCTATTTC	TCCTACCAT
8920	8930	8940	8950	8960	8970	8980	8990	9000
TCCTTTTCTC	TGAAGCGGCC	ATGACATTCC	CTTTGGCAAC	TAACGTAGAA	ACTCAACAGA	ACATTTTCT	TTCCCTAGACT	CACCTTTTAG
9010	9020	9030	9040	9050	9060	9070	9080	9090
ATGATAATGG	ACAACTATAG	ACTTGCTCAT	TGTTGAGACT	GATTGCCCT	CACCTGATC	CACCTCTGT	ATTGATGCTC	TTGGCAATTT
9100	9110	9120	9130	9140	9150	9160	9170	9180
CTTTGACTTT	CTTTTAAGG	CAGAGGCATT	TTAGTTAAT	GTAGATAAAG	AATAGTTTC	TTCCCTTCT	CCTTGGGCCA	GTTAATATT
9190	9200	9210	9220	9230	9240	9250	9260	9270
GGTCCATGGC	TACACTGCCA	CTTCCGTCCA	GTGCTGTGAT	GCCCATGACA	CCTGCAAAAT	AAGTCTGCC	TGGGCATTTT	GTACATATTA
9280	9290	9300	9310	9320	9330	9340	9350	9360
ACAGGTGAAT	TCCCGACTCT	TTTGTTTGA	ATGACAGTTC	TCATTCTTC	TATGGCTGCA	AGATGATC	AGTGTTC	ACTTACCTGA
9370	9380	9390	9400	9410	9420	9430	9440	9450
TTTGTCTGTC	GGTGGCCCCA	TATGGAACC	CTGGGTGCT	GTTGGCATAA	TAGTTTACAA	ATGGTTTTT	CAGTCTATC	CAAAATTTAT
9460	9470	9480	9490	9500	9510	9520	9530	9540

GAACCAACAA AAATATATAC TTCTGCCCTG AGATAAGCAG ATTAGCTTG TTCAATCTCT GCTTATCT CTCCATGTGG CAACATTCTG *
9550 * 9560 * 9570 * 9580 * 9590 * 9600 * 9610 * 9620 * 9630 *
TCAGCCCTCT TCATAGTGTG CAACATTTT ATCATTCTAA ATGGTCACTC TCTGCCCTTG GACCCATTTA TTATTCAACAG ATGGGGAGAA *
9640 * 9650 * 9660 * 9670 * 9680 * 9690 * 9700 * 9710 * 9720 *
CCTATCTGCA TGGACCCCTCA CCATCTCTG TGCAGCACAC ACAGTCAGG GAGCCAGTGG CGATGGCGAT GACTTCTTC CCTGGGAAT *
TCC